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OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 02:10:12 : Search time 48 Seconds
(without alignments)
121.393 Million cell updates/sec

Title: US-09-606-804-1
Perfect score: 19
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database : Issued_Patents_NA :
1: /cgn2_6/prodata/1/lna/5A.COMB.seq : *
2: /cgn2_6/prodata/1/lna/5B.COMB.seq : *
3: /cgn2_6/prodata/1/lna/6A.COMB.seq : *
4: /cgn2_6/prodata/1/lna/6B.COMB.seq : *
5: /cgn2_6/prodata/1/lna/PCUTS.COMB.seq : *
6: /cgn2_6/prodata/1/lna/Backfiles1.seq : *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	52.6	272	1	US-08-248-474-36 Sequence 36, Appl
2	10	52.6	272	3	US-08-756-849-36 Sequence 36, Appl
3	10	52.6	296	2	US-08-716-942-20 Sequence 20, Appl
4	10	52.6	296	4	US-09-130-337A-20 Sequence 20, Appl
5	10	52.6	360	6	5196523-1 Patent No. 5196523
6	10	52.6	387	4	US-08-804-372A-23 Sequence 23, Appl
7	10	52.6	382	4	US-09-404-879A-372 Sequence 372, Appl
8	10	52.6	399	6	5196523-23 Patent No. 5196523
9	10	52.6	421	1	US-08-609-657-15 Sequence 15, Appl
10	10	52.6	424	6	5196523-23 Patent No. 5196523
11	10	52.6	467	4	US-09-257-584-8 Sequence 8, Appl
12	10	52.6	531	4	US-09-222-575-123 Sequence 123, Appl
13	10	52.6	754	4	US-09-020-956-20 Sequence 20, Appl
14	10	52.6	754	4	US-09-030-607-20 Sequence 20, Appl
15	10	52.6	754	4	US-09-605-785-20 Sequence 20, Appl
16	10	52.6	754	4	US-09-439-313-20 Sequence 20, Appl
17	10	52.6	754	4	US-09-352-616A-20 Sequence 20, Appl
18	10	52.6	754	4	US-09-232-149A-20 Sequence 20, Appl
19	10	52.6	843	4	US-09-171-209-38 Sequence 38, Appl
20	10	52.6	849	4	US-08-998-416-552 Sequence 552, Appl
21	10	52.6	904	4	US-09-541-941B-21 Sequence 21, Appl
22	10	52.6	1050	4	US-09-137-855-1 Sequence 5, Appl
23	10	52.6	1117	4	US-09-347-819-5 Sequence 1855, Appl
24	10	52.6	1137	4	US-09-134-001C-1855 Sequence 27, Appl
25	10	52.6	1137	4	US-09-541-941B-27 Sequence 7, Appl
26	10	52.6	1347	2	US-08-286-819A-7 Sequence 31, Appl
27	10	52.6	1347	2	US-08-286-819A-31 Sequence 31, Appl

28	10	52.6	1347	3	US-08-980-357-7 Sequence 7, Appl
29	10	52.6	1347	3	US-08-980-357-31 Sequence 31, Appl
30	10	52.6	1377	4	US-09-134-001C-1389 Sequence 1389, Ap
31	10	52.6	1545	2	US-08-660-963-9 Sequence 9, Appl
32	10	52.6	1617	2	US-08-467-963C-25 Sequence 25, Appl
33	10	52.6	1617	2	US-08-838-189D-25 Sequence 25, Appl
34	10	52.6	1617	3	US-08-852-344D-25 Sequence 25, Appl
35	10	52.6	1617	3	US-08-344-639E-25 Sequence 25, Appl
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37	10	52.6	1763	4	US-09-348-443-1 Sequence 1, Appl
38	10	52.6	1763	6	5185262-1 Patent No. 5185262
39	10	52.6	1770	3	US-09-006-636-1 Sequence 1, Appl
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41	10	52.6	1770	4	US-09-006-632-1 Sequence 1, Appl
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43	10	52.6	1770	4	US-09-325-274-1 Sequence 1, Appl
44	10	52.6	1770	4	US-09-325-274-1 Sequence 1, Appl
45	10	52.6	1844	2	US-08-467-963C-1 Sequence 1, Appl
46	10	52.6	1844	2	US-08-838-189D-1 Sequence 1, Appl
47	10	52.6	1844	3	US-08-852-344D-1 Sequence 1, Appl
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49	10	52.6	1844	4	US-08-467-969A-1 Sequence 1, Appl
50	10	52.6	1844	4	US-08-467-961A-1 Sequence 1, Appl
51	10	52.6	1844	4	US-08-001-554A-1 Sequence 1, Appl
52	10	52.6	1897	4	US-09-167-322-10 Sequence 10, Appl
53	10	52.6	1972	4	US-09-370-098-1 Sequence 1, Appl
54	10	52.6	1992	4	US-09-484-970B-150 Sequence 150, App
55	10	52.6	2034	4	US-08-464-601-1 Sequence 1, Appl
56	10	52.6	2034	4	US-09-210-993A-1 Sequence 1, Appl
57	10	52.6	2034	4	US-09-939-573-1 Sequence 1, Appl
58	10	52.6	2298	1	US-07-917-722-1 Sequence 1, Appl
59	10	52.6	2298	1	US-08-478-086-1 Sequence 1, Appl
60	10	52.6	2298	5	US-09-061-304-1 Sequence 1, Appl
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62	10	52.6	2310	3	US-08-458-444A-1 Sequence 1, Appl
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67	10	52.6	2319	4	US-08-484-939A-1 Sequence 1, Appl
68	10	52.6	2363	1	US-07-923-724-7 Sequence 7, Appl
69	10	52.6	2363	2	US-08-609-426A-7 Sequence 7, Appl
70	10	52.6	2379	2	US-08-374-652C-1 Sequence 1, Appl
71	10	52.6	2458	2	US-08-756-806A-65 Sequence 65, Appl
72	10	52.6	2458	4	US-09-143-214-65 Sequence 29, Appl
73	10	52.6	2458	4	US-09-506-073-29 Sequence 29, Appl
74	10	52.6	2588	4	US-09-087-465-7 Sequence 7, Appl
75	10	52.6	2606	1	US-08-408-318-1 Sequence 1, Appl
76	10	52.6	2606	1	US-08-839-164-1 Sequence 1, Appl
77	10	52.6	2818	4	US-09-221-017B-506 Sequence 506, Appl
78	10	52.6	2885	2	US-08-791-849A-15 Sequence 15, Appl
79	10	52.6	3061	1	US-09-570-842-1 Sequence 1, Appl
80	10	52.6	3061	1	US-08-700-576-1 Sequence 1, Appl
81	10	52.6	3280	4	US-09-484-970B-43 Sequence 43, Appl
82	10	52.6	3292	1	US-07-814-964-12 Sequence 12, Appl
83	10	52.6	3292	1	US-08-258-442-12 Sequence 12, Appl
84	10	52.6	3292	1	US-08-328-809-7 Sequence 7, Appl
85	10	52.6	3292	5	PCT-US92-11107-12 Sequence 12, Appl
86	10	52.6	3420	3	US-09-039-859-8 Sequence 8, Appl
87	10	52.6	3720	4	US-09-342-681C-12 Sequence 12, Appl
88	10	52.6	3736	4	US-09-600-776-10 Sequence 10, Appl
89	10	52.6	3981	3	US-09-008-979A-7 Sequence 7, Appl
90	10	52.6	3981	4	US-09-460-618-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-248-474-36
Sequence 36, Application US/08248474
Patent No. 5612471
GENERAL INFORMATION:

```

APPLICANT: MCK, BIRD, David
APPLICANT: WILSON, Mark A.
TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
CITY: Stuart Street Tower, One Market Plaza
STATE: San Francisco
COUNTRY: California
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,474
FILING DATE: 25-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-535
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..272
OTHER INFORMATION: /standard_name="DB# 155"
US-08-248-474-36

Query Match
Best Local Similarity 52.6%; Score 10; DB 1; Length 272;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
DB 97 CCAATATTATTTCACG 115

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,849
FILING DATE: 26-NOV-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,474
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-053510US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..272
OTHER INFORMATION: /standard_name="DB# 155"
US-08-756-849-36

Query Match
Best Local Similarity 52.6%; Score 10; DB 3; Length 272;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
DB 97 CCAATATTATTTCACG 115

RESULT 3
US-08-716-942-20/C
Sequence 20, Application US/08/716942
Patent No. 5849491
GENERAL INFORMATION:
APPLICANT: Terragen Diversity Inc.
APPLICANT: Radomski, Christopher C. A.
APPLICANT: Seow, Kah Tong
APPLICANT: Warren, R. Anthony J.
TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENE
TITLE OF INVENTION: SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
STATE: NY
COUNTRY: USA
ZIP: 10598-4412
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,942
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004,157
FILING DATE: 20-SEP-95
ATTORNEY/AGENT INFORMATION:
NAME: Marina T. Larson

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: REGISTRATION NUMBER: 32,038
: REFERENCE/DOCKET NUMBER: TERR.P-001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (914) 245-3252
: TELEFAX: (914) 962-4330
: TELEX:
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 296
: TYPE: nucleic acid
: STRANDEDNESS: DOUBLE
: TOPOLOGY: linear
: MOLECULE TYPE: genomic DNA
: HYPOTHETICAL: no
: ANTI-SENSE: no
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
: ORGANISM:
: FEATURE:
: NAME/KEY: fragment of xylanase gene from degenerate primer
: US-08-716-942-20
:
: Query Match 52.6%; Score 10; DB 2; Length 296;
: Best Local Similarity 52.6%; Pred. No. 3.7e+02;
: Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 217 CCAATGTTGTGGCCACG 199

RESULT 4
US-09-130-337A-20/c
: Sequence 20, Application US/09130337A
: Patent No. 6441148
: GENERAL INFORMATION:
: APPLICANT: Radomski, CCA
: APPLICANT: Seow, KT
: APPLICANT: Warren, RAJ
: TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
: TITLE OF INVENTION: FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIO
: TITLE OF INVENTION: THEREBY
: FILE REFERENCE: 9993-004
: CURRENT APPLICATION NUMBER: US/09/130,337A
: CURRENT FILING DATE: 1998-08-06
: PRIOR APPLICATION NUMBER: 08/716,942
: PRIOR FILING DATE: 1996-09-20
: PRIOR APPLICATION NUMBER: 60/004,157
: PRIOR FILING DATE: 1995-09-22
: NUMBER OF SEQ ID NOS: 25
: SEQ ID NO 20
: LENGTH: 296
: TYPE: DNA
: ORGANISM: Unknown organism
: FEATURE:
: OTHER INFORMATION: Description of unknown organism: soil microbe
: US-09-130-337A-20

Query Match 52.6%; Score 10; DB 4; Length 296;
Best Local Similarity 52.6%; Pred. No. 3.7e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 217 CCAATGTTGTGGCCACG 199

RESULT 5
5196523-1
: Patent No. 5196523
: APPLICANT: LEE, AMY S.
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: TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
: CALCIUM AND TEMPERATURE
: NUMBER OF SEQUENCES: 28
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/354,988
: FILING DATE: 19-MAY-1989
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 282,880
: FILING DATE: 05-DEC-1988
: APPLICATION NUMBER: 690,951
: FILING DATE: 01-JAN-1985
: SEQ ID NO:1:
: LENGTH: 360
: 5196523-1

Query Match 52.6%; Score 10; DB 6; Length 360;
Best Local Similarity 52.6%; Pred. No. 3.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 282 CCAATCGAGAGCCTCCACG 300
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RESULT 6
US-08-804-372A-23
: Sequence 23, Application US/08804372A
: Patent No. 6183753
: GENERAL INFORMATION:
: APPLICANT: Cochran, Mark D.
: APPLICANT: Wild, Martha A.
: APPLICANT: Winslow, Barbara J.
: TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
: TITLE OF INVENTION: Thereof
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/804,372A
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 2552/39115E
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 387 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: US-08-804-372A-23

Query Match 52.6%; Score 10; DB 4; Length 387;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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QY 1 CCAATNNNNNNNNCCAG 19
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Db 262 CCAATCAAAAGCTGCCAG 280

RESULT 7
US-09-404-879A-372/C

; Sequence 372, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-404-879A-372

Query Match 52.6%; Score 10; DB 4; Length 392;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
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Db 37 CCAATCCAGAGCTCCAG 19

RESULT 8
5196523-23
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO: 23
; LENGTH: 399
5196523-23

Query Match 52.6%; Score 10; DB 6; Length 399;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
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Db 311 CCAATCGAGGCTCCAG 329

RESULT 9
5196523-22
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO: 22
; LENGTH: 421
5196523-22

Query Match 52.6%; Score 10; DB 6; Length 421;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
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Db 311 CCAATCGGCGGCTCCAG 329

RESULT 10
US-08-609-657-15

; Sequence 15, Application US/08609657
; Patent No. 5681706
; GENERAL INFORMATION:
; APPLICANT: Anderson, Garth R.
; APPLICANT: Estes, Scott D.
; APPLICANT: Stoler, Daniel L.
; TITLE OF INVENTION: Mammalian Anoxia-Responsive Regulatory
; TITLE OF INVENTION: Element
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One Mt Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: Wordperfect for Windows 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,657
; FILING DATE: 01 March 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, M. Bud
; REGISTRATION NUMBER: 35,300
; REFERENCE/DOCKET NUMBER: 03551,0017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 856-4000
; TELEFAX: (716) 849-0349
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
US-08-609-657-15

Query Match 52.6%; Score 10; DB 1; Length 424;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAG 19
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Db 361 CCAATTGATGTACCAG 379

RESULT 11
US-09-257-584-8/C
; Sequence 8, Application US/09257584A

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Patent No. 6177611
GENERAL INFORMATION:
APPLICANT: Rice, Douglas A.
FILE REFERENCE: 5718-33, 035718/175218
CURRENT APPLICATION NUMBER: US/09/257,584A
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 60/076,075
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 467
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: cab-10 promoter
NAME/KEY: unsure
LOCATION: (370)
OTHER INFORMATION: Nucleotide at this position may be a or g or c or
US-09-257-584-8

Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 467;
Pred. No. 4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 266 CCAATCACCTCTCCACG 248

RESULT 12
US-09-222-575-123
Sequence 123, Application US/09222575
GENERAL INFORMATION:
APPLICANT: Yuglu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
FILE REFERENCE: 210121.470
CURRENT APPLICATION NUMBER: US/09/222,575
CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 123
LENGTH: 531
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: modified_base
LOCATION: (152)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (482)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
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NAME/KEY: modified_base
LOCATION: (502)
OTHER INFORMATION: where n is a, c, g or t
US-09-222-575-123
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 4; Length 531;
Pred. No. 4.1e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    ||||| |||||
Db 506 CCAATTTCAGCACCACG 524

RESULT 13
US-09-020-956-20
Sequence 20, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-020-956-20

Query Match
Best Local Similarity 57.9%; Score 10; DB 4; Length 754;
Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
    ||||| | |||||
Db 303 CCAATTGTTTNGCCACG 321

RESULT 14
US-09-030-607-20
Sequence 20, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
```

STATE: MA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 754 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-030-607-20

Query Match 52.6%; Score 10; DB 4; Length 754;
Best Local Similarity 57.9%; Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 303 CCAATGCTTTTNGCCACG 321

RESULT 15
US-09-605-785-20
Sequence 20, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolck, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(754)

OTHER INFORMATION: n = A,T,C or G
US-09-605-785-20

Query Match 52.6%; Score 10; DB 4; Length 754;
Best Local Similarity 57.9%; Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 303 CCAATGCTTTTNGCCACG 321

RESULT 16
US-09-439-313-20
Sequence 20, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(754)
OTHER INFORMATION: n = A,T,C or G
US-09-439-313-20

Query Match 52.6%; Score 10; DB 4; Length 754;
Best Local Similarity 57.9%; Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 303 CCAATGCTTTTNGCCACG 321

RESULT 17
US-09-352-616A-20
Sequence 20, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqi
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754

```

: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(754)
: OTHER INFORMATION: n = A,T,C or G
US-09-352-615A-20

```

```

Query Match          52.6%; Score 10; DB 4; Length 754;
Best Local Similarity 57.9%; Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 1 CCAATNNNNNNNNCCAGC 19
    ||||| 1 |||||
Db 303 CCAATTGTTTNGCCAGC 321

```

```

RESULT 18
US-09-232-149A-20
: Sequence 20, Application US/09232149A
: Patent No. 6465611
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
: FILE REFERENCE: 210121.427C6
: CURRENT APPLICATION NUMBER: US/09/232,149A
: CURRENT FILING DATE: 1999-01-15
: NUMBER OF SEQ ID NOS: 338
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 20
: LENGTH: 754
: TYPE: DNA
: ORGANISM: Homo sapien
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(754)
: OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-20

```

```

Query Match          52.6%; Score 10; DB 4; Length 754;
Best Local Similarity 57.9%; Pred. No. 4.3e+02;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 1 CCAATNNNNNNNNCCAGC 19
    ||||| 1 |||||
Db 303 CCAATTGTTTNGCCAGC 321

```

```

RESULT 19
US-09-171-209-38
: Sequence 38, Application US/09171209
: Patent No. 6448000
: GENERAL INFORMATION:
: APPLICANT: VANDERBILT UNIVERSITY
: APPLICANT: 305 Kirkland Hall
: Nashville, TN 37240
: TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
: INFECTION
: NUMBER OF SEQUENCES: 83
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Needle & Rosenberg, P.C.
: STREET: 127 Peachtree Street, Suite 1200
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30303-1811
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/171,209
: FILING DATE: 08-Mar-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US97/06067
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Selby, Elizabeth
: REGISTRATION NUMBER: 38,298
: REFERENCE/DOCKET NUMBER: 22000.0061/P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 404 688 0770
: TELEFAX: 404 688 9880
: INFORMATION FOR SEQ ID NO: 38:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 843 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-171-209-38

```

```

Query Match          52.6%; Score 10; DB 4; Length 843;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

QY 1 CCAATNNNNNNNNCCAGC 19
    ||||| 1 |||||
Db 638 CCAATTGTATGTAACCCAGC 656

```

```

RESULT 20
US-08-998-416-552
: Sequence 552, Application US/08998416
: Patent No. 6239264
: GENERAL INFORMATION:
: APPLICANT: Philippen, Peter
: APPLICANT: Pohlmann, Rainer
: APPLICANT: Steiner, Sabine
: APPLICANT: Mohr, Christine
: APPLICANT: Wendland, Jurgen
: APPLICANT: Knechtle, Philipp
: APPLICANT: Redischung, Corinne
: TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
: AND USES THEREOF
: NUMBER OF SEQUENCES: 1152
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: No. 6239264artis Corporation
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NO. 6239264th Carolina
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/998,416
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: CH 0016/97
: FILING DATE: 31-DEC-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
: TELECOMMUNICATION INFORMATION:

```

TELEPHONE: 919-541-8587
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 552:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 849 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE:
 ORGANISM: PAG1384UP
 US-08-998-416-552

Query Match 52.6%; Score 10; DB 4; Length 849;
 Best Local Similarity 57.9%; Pred. No. 4.4e+02;
 Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 Db 690 CCAATATACCTGCTCCACG 708

RESULT 21
 US-09-541-941B-21/C
 Sequence 21, Application US/09541941B
 Patent No. 6309840
 GENERAL INFORMATION:
 APPLICANT: Wang, Jun
 APPLICANT: Shaw, Pang Chui
 APPLICANT: Paul, Pul-Hay
 APPLICANT: Ngan, But-and Fai Ngor Karenda Ngan
 TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH
 FILE REFERENCE: 2913/52188-2A
 CURRENT APPLICATION NUMBER: US/09/541,941B
 CURRENT FILING DATE: 2000-04-03
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 21
 LENGTH: 904
 TYPE: DNA
 ORGANISM: Campanumoea Javanica Blume
 US-09-541-941B-21

Query Match 52.6%; Score 10; DB 4; Length 904;
 Best Local Similarity 52.6%; Pred. No. 4.4e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 Db 646 CCAATATCCCTCCACG 628

RESULT 22
 US-09-137-855-1/C
 Sequence 1, Application US/09137855B
 Patent No. 6242237
 GENERAL INFORMATION:
 APPLICANT: Kotod, Lene V.
 APPLICANT: Kaupinen, Markus S.
 APPLICANT: Andersen, Lene N.
 APPLICANT: Clausen, Ib G.
 APPLICANT: Molleretz, Anette
 TITLE OF INVENTION: An Enzyme With Galactanase Activity
 FILE REFERENCE: 4686.204-US
 CURRENT APPLICATION NUMBER: US/09/137,855B
 CURRENT FILING DATE: 1998-08-21
 EARLIER APPLICATION NUMBER: 0233/96
 EARLIER FILING DATE: 1996-03-01
 EARLIER APPLICATION NUMBER: 0235/96
 EARLIER FILING DATE: 1996-03-01
 EARLIER APPLICATION NUMBER: PCT/DK97/00092
 EARLIER FILING DATE: 1997-02-28

NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 1
 LENGTH: 1050
 TYPE: DNA
 ORGANISM: Myceliophthora thermophila
 US-09-137-855-1

Query Match 52.6%; Score 10; DB 4; Length 1050;
 Best Local Similarity 52.6%; Pred. No. 4.6e+02;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 Db 798 CCAATGCTCGACACG 780

RESULT 23
 US-09-347-819-5/C
 Sequence 5, Application US/09347819
 Patent No. 6184036
 GENERAL INFORMATION:
 APPLICANT: Cahoon, Rebecca E.
 APPLICANT: Rafalski, J. Antoni
 APPLICANT: Falco, S. Carl
 TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
 FILE REFERENCE: BB-1174-C
 CURRENT APPLICATION NUMBER: US/09/347,819
 CURRENT FILING DATE: 1999-07-02
 EARLIER APPLICATION NUMBER: 60/093,209
 EARLIER FILING DATE: JULY 17, 1998
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 5
 LENGTH: 1117
 TYPE: DNA
 ORGANISM: Oryza sativa

FEATURE:
 NAME/KEY: unsure
 LOCATION: (225)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (227)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (229)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (246)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (255)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (308)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (320)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1043)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1068)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1070)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1084)
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1100)

FEATURE:
NAME/KEY: unsure
LOCATION: (1114)
FEATURE:
NAME/KEY: unsure
LOCATION: (1116)
US-09-347-819-5

Query Match 52.6%; Score 10; DB 4; Length 1117;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
11111
Db 769 CCAATGGGCCAAACCACG 751

RESULT 24
US-09-134-001C-1855/C
Sequence 1855, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1855
LENGTH: 1137
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1855

Query Match 52.6%; Score 10; DB 4; Length 1137;
Best Local Similarity 52.6%; Pred. No. 4.6e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
11111
Db 683 CCAATAGCTCTATTCACG 665

RESULT 25
US-09-541-941B-27/C
Sequence 27, Application US/09541941B
Patent No. 6309840
GENERAL INFORMATION:
APPLICANT: Wang, Jun
APPLICANT: Shaw, Pang Chun
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH
TITLE OF INVENTION: FOR THE AUTHENTICATION OF HERBAL CHINESE MEDICINES
FILE REFERENCE: 2913/52188-2A
CURRENT APPLICATION NUMBER: US/09/541,941B
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 1193
TYPE: DNA
ORGANISM: Pheretima Aspergillus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (100)..(100)
OTHER INFORMATION: n = a, t, c, g, or u
US-09-541-941B-27

Query Match 52.6%; Score 10; DB 4; Length 1193;
Best Local Similarity 52.6%; Pred. No. 4.7e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
11111
Db 24 CCAATGGTAGGACGACG 6

RESULT 26
US-08-286-819A-7
Sequence 7, Application US/08286819A
Patent No. 5871910

GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COURVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S.
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,819A
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELETYPE: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

LOCATION: 215..1243
US-08-286-819A-7

Query Match 52.6%; Score 10; DB 2; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
db 961 CCAATTATATCAGCCACG 979

RESULT 27

US-08-286-819A-31
Sequence 31, Application US/08286819A
Patent No. 5871910

GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL

APPLICANT: DUKTA-MALEN, SYLVIE

APPLICANT: MOLINAS, CATHERINE

APPLICANT: COURVALIN, PATRICE

TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR

TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/286,819A

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/174,682

FILING DATE: 28-DEC-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/917,146

FILING DATE: 10-AUG-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR/91/00855

FILING DATE: 29-OCT-1991

APPLICATION NUMBER: FR 9013579

FILING DATE: 31-OCT-1990

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5871910man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 660-060-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 1347 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: linear

US-08-236-819A-31

Query Match 52.6%; Score 10; DB 2; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
db 961 CCAATTATATCAGCCACG 979

RESULT 28

US-08-980-357-7
Sequence 7, Application US/08980357
Patent No. 6013508

GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL

APPLICANT: DUKTA-MALEN, SYLVIE

APPLICANT: MOLINAS, CATHERINE

APPLICANT: COURVALIN, PATRICE

TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR

TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/980,357

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,819

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/917,146

FILING DATE: 10-AUG-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR/91/00855

FILING DATE: 29-OCT-1991

APPLICATION NUMBER: FR 9013579

FILING DATE: 31-OCT-1990

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 6013508man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 660-060-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1347 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

US-08-236-819A-31

Query Match 52.6%; Score 10; DB 2; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
db 961 CCAATTATATCAGCCACG 979

RESULT 28

US-08-980-357-7
Sequence 7, Application US/08980357
Patent No. 6013508

GENERAL INFORMATION:

APPLICANT: ARTHUR, MICHEL

APPLICANT: DUKTA-MALEN, SYLVIE

APPLICANT: MOLINAS, CATHERINE

APPLICANT: COURVALIN, PATRICE

TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR

TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/980,357

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,819

FILING DATE: 05-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/917,146

FILING DATE: 10-AUG-1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR/91/00855

FILING DATE: 29-OCT-1991

APPLICATION NUMBER: FR 9013579

FILING DATE: 31-OCT-1990

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 6013508man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 660-060-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1347 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

LOCATION: 215.1243
US-08-980-357-7

Query Match 52.6%; Score 10; DB 3; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 961 CCAATTATCAGCCGACG 979

RESULT 29
US-08-980-357-31
Sequence 31, Application US/08980357
Patent No. 6013508
GENERAL INFORMATION:
APPLICANT: ARTHUR, MICHEL
APPLICANT: DUKTA-MALEN, SYLVIE
APPLICANT: MOLINAS, CATHERINE
APPLICANT: COUBVALIN, PATRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYMERES, IN PARTICULAR
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,819
FILING DATE: 05-AUG-1994
APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,146
FILING DATE: 10-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9013579
FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: OHLON, NO. 6013508man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-060-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-980-357-31

Query Match 52.6%; Score 10; DB 3; Length 1347;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

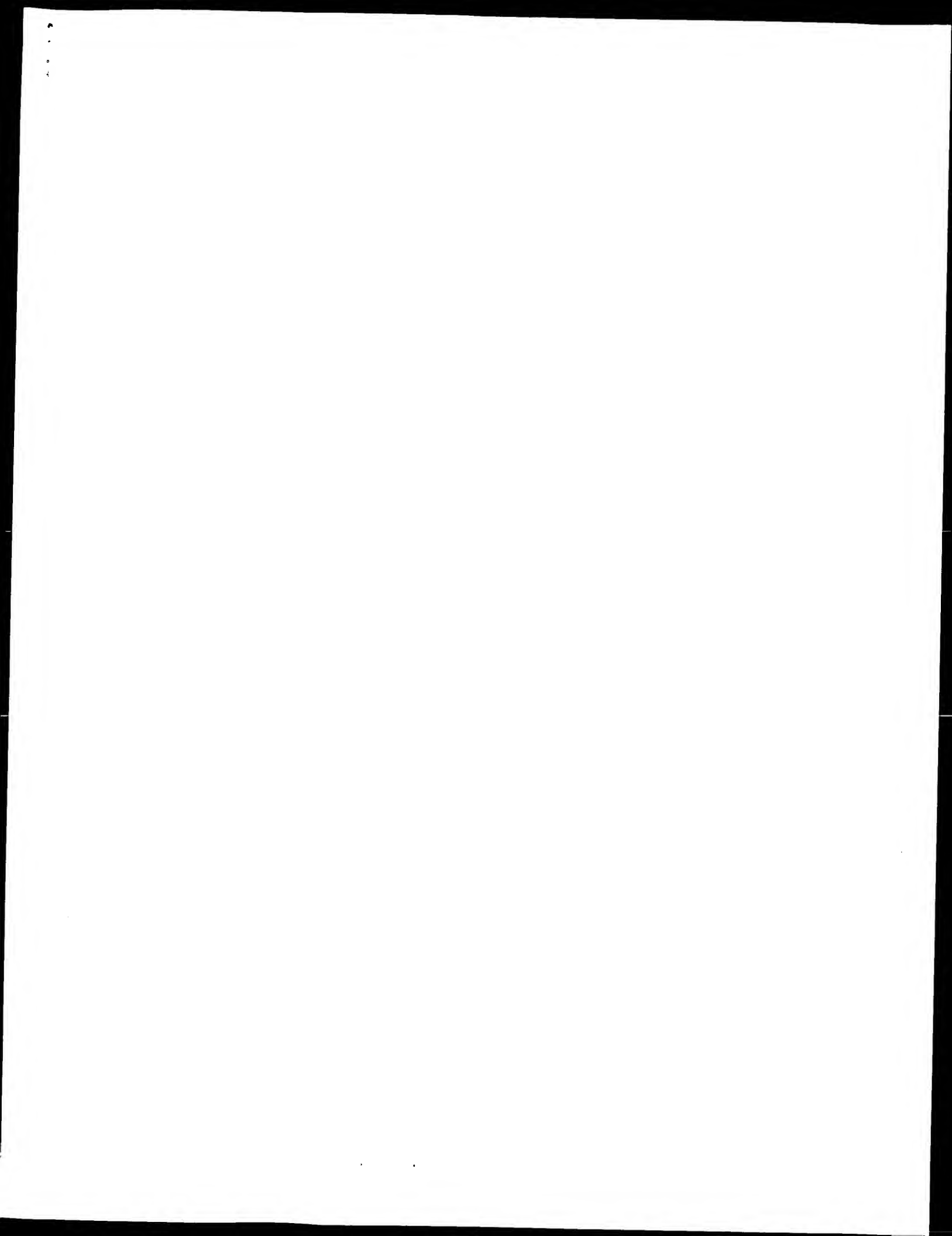
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RESULT 30
US-09-134-001C-1389
Sequence 1389, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1389
LENGTH: 1377
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1389

Query Match 52.6%; Score 10; DB 4; Length 1377;
Best Local Similarity 52.6%; Pred. No. 4.8e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAG 19
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Db 428 CCAATCTGATTACGACG 446

Search completed: November 16, 2002, 03:33:38
Job Time : 50 secs



GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 01:20:22 ; Search time 2576 Seconds
(without alignments)
214.656 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

Database :

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1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
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16: em_fun: *
17: em_hum: *
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19: em_mu: *
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28: em_un: *
29: em_vl: *
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32: em_hlg_other: *
33: em_hlg_mus: *
34: em_hlg_pln: *
35: em_hlg_rod: *
36: em_hlg_man: *
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41: em_hlgc_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	10	52.6	19 6 AX275341	AX275341 Sequence
2	10	52.6	19 6 E28797	E28797 Endoplasmic
3	10	52.6	19 6 E28801	E28801 Endoplasmic
4	10	52.6	19 6 E28802	E28802 Endoplasmic
5	10	52.6	19 6 E28803	E28803 Endoplasmic
6	10	52.6	19 6 E28804	E28804 Endoplasmic
7	10	52.6	19 6 E28805	E28805 Endoplasmic
8	10	52.6	19 6 E28806	E28806 Endoplasmic
9	10	52.6	19 6 E28807	E28807 Endoplasmic
10	10	52.6	19 6 E28808	E28808 Endoplasmic
11	10	52.6	19 6 E28809	E28809 Endoplasmic
12	10	52.6	19 6 E44202	E44202 Endoplasmic
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18	10	52.6	19 6 E44211	E44211 Endoplasmic
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20	10	52.6	19 6 E44213	E44213 Endoplasmic
21	10	52.6	19 6 E44214	E44214 Endoplasmic
22	10	52.6	24 6 AX443752	AX443752 Sequence
23	10	52.6	25 6 AX447733	AX447733 Sequence
24	10	52.6	29 6 E44234	E44234 Endoplasmic
25	10	52.6	99 9 HUMCG3A02	HUMCG3A02 Human alpha
26	10	52.6	105 8 AF479941	AF479941 Saccharom
27	10	52.6	112 6 AX343726	AX343726 Sequence
28	10	52.6	122 6 E28800	E28800 Endoplasmic
29	10	52.6	122 6 E44205	E44205 Endoplasmic
30	10	52.6	125 14 AF271990	AF271990 Human ade
31	10	52.6	127 6 AX343728	AX343728 Sequence
32	10	52.6	136 6 AX033516	AX033516 Sequence
33	10	52.6	136 6 AX033517	AX033517 Sequence
34	10	52.6	142 6 AX033504	AX033504 Sequence
35	10	52.6	143 6 AX033505	AX033505 Sequence
36	10	52.6	143 9 HUMETG05	HUMETG05 Homo sapien
37	10	52.6	145 6 AX072778	AX072778 Sequence
38	10	52.6	149 6 AX033508	AX033508 Sequence
39	10	52.6	150 6 AX033507	AX033507 Sequence
40	10	52.6	153 3 AF305966	AF305966 Haemonchu
41	10	52.6	169 10 AY029607S2	AY029607 Mesocric
42	10	52.6	189 8 DO412LMS2	DO412LMS2 Mesocric
43	10	52.6	195 6 AX310584	AX310584 Sequence
44	10	52.6	204 8 AF229112S3	AF229112 Downingia
45	10	52.6	205 6 AX386623	AX386623 Sequence
46	10	52.6	210 6 AX439681	AX439681 Sequence
47	10	52.6	214 6 AX156202	AX156202 Sequence
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50	10	52.6	220 6 AX313758	AX313758 Sequence
51	10	52.6	224 8 AF229145	AF229145 Downingia
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53	10	52.6	225 8 AF229139	AF229139 Downingia
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66 10 52.6 272 6 AR104623
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 79 10 52.6 304 9 HS42GARC
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 83 10 52.6 313 11 AU029237
 84 10 52.6 315 1 NMU06748
 85 10 52.6 320 4 AFU03597
 86 10 52.6 326 4 LMU03587
 87 10 52.6 326 4 PVU03596
 88 10 52.6 326 4 HU003598
 89 10 52.6 328 1 AF092218
 90 10 52.6 331 4 CFU03585

ALIGNMENTS

RESULT 1
 AX275341
 LOCUS AX275341 19 bp DNA linear PAT 29-OCT-2001
 DEFINITION Sequence 1 from Patent WO0171018.
 AX275341 GI:16547677

REFERENCE
 AUTHORS Hermonat, P.L., Mane, M. and Liu, Y.
 TITLE Secreting products from skin by adeno-associated virus (aav) gene transfer
 JOURNAL Patent: WO 0171018-A 1 27-SEP-2001;
 THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)
 FEATURES
 source location/Qualifiers
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 /organism="unidentified"
 /db_xref="taxon:32644"
 /note="glucose response element"
 BASE COUNT 3 a 5 c 1 g 9 others
 ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCAATNNNNNNNNCCAGC 19
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 DB 1 CCAATNNNNNNNNCCAGC 19
 RESULT 2
 E28797 19 bp DNA linear PAT 18-JUN-2001
 LOCUS E28797
 DEFINITION Endoplasmic reticulum stress-response regulatory element.
 E28797
 ACCESSION E28797
 VERSION E28797.1 GI:13020851
 KEYWORDS JP 1999243959-A/1.
 SOURCE unidentified.
 ORGANISM unidentified.
 unclassified.

REFERENCE
 AUTHORS Hideo, Y., Hideki, Y. and Takashi, Y.
 TITLE Endoplasmic reticulum stress-response regulatory element
 JOURNAL Patent: JP 1999243959-A 1 14-SEP-1999;
 HSP RESEARCH INST INC
 COMMENT
 OS Unidentified
 PN JP 1999243959-A/1
 PD 14-SEP-1999
 PR 04-MAR-1998 JP 1998052453

PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
 PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, C12N15/00,
 PC A61K37/02
 CC Strandedness: Double;
 CC Topology: Linear;
 FH Key
 FT enhancer
 location/Qualifiers
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 /db_xref="taxon:32644"

BASE COUNT 3 a 5 c 1 g 1 t 9 others
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 Query Match 52.6%; Score 10; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAGC 19
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 DB 1 CCAATNNNNNNNNCCAGC 19

RESULT 3
 E28801 19 bp DNA linear PAT 18-JUN-2001
 LOCUS E28801
 DEFINITION Endoplasmic reticulum stress-response regulatory element.
 E28801
 ACCESSION E28801.1 GI:13020855
 VERSION JP 1999243959-A/5.
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 REFERENCE
 AUTHORS Hideo, Y., Hideki, Y. and Takashi, Y.
 TITLE Endoplasmic reticulum stress-response regulatory element
 JOURNAL Patent: JP 1999243959-A 5 14-SEP-1999;
 HSP RESEARCH INST INC
 OS Homo sapiens (human)
 PN JP 1999243959-A/5
 PD 14-SEP-1999
 PR 04-MAR-1998 JP 1998052453

PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
 PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
 PC A61K37/02
 CC Strandedness: Double;
 CC Topology: Linear;
 FH Key
 FT enhancer
 location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 3 a 9 c 5 g 2 t
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Query Match 52.6%; Score 10; DB 6; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Db 1 CCAATCGCGCGCTCCACG 19

RESULT 4

E28802 19 bp DNA linear PAT 18-JUN-2001
LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28802
ACCESSION E28802.1 GI:13020856
VERSION JP 1999243959-A/6.
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
Hideo, Y., Hideki, Y. and Takashi, Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 6 14-SEP-1999;
HSP RESEARCH INST INC

COMMENT

OS Mus sp. (mouse)
PN JP 1999243959-A/6
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453

PR HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PI C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH key enhancer
FT location/Qualifiers

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/db_xref="taxon:10095"

BASE COUNT 4 a 8 c 5 g 2 t
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Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 1 CCAATCGCGCGCTCCACG 19

RESULT 5
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LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28803
ACCESSION E28803.1 GI:13020857
VERSION JP 1999243959-A/7.
KEYWORDS
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 19)
Hideo, Y., Hideki, Y. and Takashi, Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 7 14-SEP-1999;
HSP RESEARCH INST INC

COMMENT

OS Rattus sp. (rat)
PN JP 1999243959-A/7
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453

PR HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PI C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
PC A61K37/02

CC Strandedness: Double;
CC Topology: Linear;
FH key enhancer
FT location/Qualifiers

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ORIGIN

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Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATCGCGCGCTCCACG 19

RESULT 6
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LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28804
ACCESSION E28804.1 GI:13020858
VERSION JP 1999243959-A/8.
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 19)
Hideo, Y., Hideki, Y. and Takashi, Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 8 14-SEP-1999;
HSP RESEARCH INST INC

COMMENT

OS Homo sapiens (human)
PN JP 1999243959-A/8
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453

PR HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PI C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
PC A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH key enhancer
FT location/Qualifiers

FEATURES
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/organism="Homo sapiens"
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BASE COUNT 4 a 10 c 4 g 1 t
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Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
Db 1 CCAATCGCGCGCTCCACG 19

RESULT 7
E28805 19 bp DNA linear PAT 18-JUN-2001
LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28805
ACCESSION E28805.1 GI:13020859
VERSION JP 1999243959-A/9.
KEYWORDS
SOURCE Gallus sp.
ORGANISM Gallus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 1 (bases 1 to 19)
 Hideo, Y., Hideki, Y. and Takashi, Y.
 Endoplasmic reticulum stress-response regulatory element
 Patent: JP 199243959-A 9 14-SEP-1999;
 HSP RESEARCH INST INC
 OS Gallus sp. (chicken)
 PN JP 199243959-A/9
 PD 14-SEP-1999
 PR 04-MAR-1998 JP 1998052453
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 QY 1 CCAATNNNNNNNNCCACG 19
 1 11111 11111
 Db 1 CCAATCGAGCGCCGACG 19
 RESULT 8
 LOCUS E28806 19 bp DNA linear PAT 18-JUN-2001
 DEFINITION Endoplasmic reticulum stress-response regulatory element.
 ACCESSION E28806
 VERSION E28806.1 GI:13020860
 KEYWORDS JP 199243959-A/10.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 19)
 Hideo, Y., Hideki, Y. and Takashi, Y.
 Endoplasmic reticulum stress-response regulatory element
 Patent: JP 199243959-A 10 14-SEP-1999;
 HSP RESEARCH INST INC
 OS Homo sapiens (human)
 PN JP 199243959-A/10
 PD 14-SEP-1999
 PR 04-MAR-1998 JP 1998052453
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Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCAATNNNNNNNNCCACG 19
 1 11111 11111
 Db 1 CCAATCGAGCGCCGACG 19
 RESULT 9
 LOCUS E28807 19 bp DNA linear PAT 18-JUN-2001
 DEFINITION Endoplasmic reticulum stress-response regulatory element.
 ACCESSION E28807
 VERSION E28807.1 GI:13020861
 KEYWORDS JP 199243959-A/11.
 SOURCE Gallus sp.
 ORGANISM Gallus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 1 (bases 1 to 19)
 Hideo, Y., Hideki, Y. and Takashi, Y.
 Endoplasmic reticulum stress-response regulatory element
 Patent: JP 199243959-A 11 14-SEP-1999;
 HSP RESEARCH INST INC
 OS Gallus sp. (chicken)
 PN JP 199243959-A/11
 PD 14-SEP-1999
 PR 04-MAR-1998 JP 1998052453
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 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCAATNNNNNNNNCCACG 19
 1 11111 11111
 Db 1 CCAATCGAGCGCCGACG 19
 RESULT 10
 LOCUS E28808 19 bp DNA linear PAT 18-JUN-2001
 DEFINITION Endoplasmic reticulum stress-response regulatory element.
 ACCESSION E28808
 VERSION E28808.1 GI:13020862
 KEYWORDS JP 199243959-A/12.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 19)
 Hideo, Y., Hideki, Y. and Takashi, Y.
 Endoplasmic reticulum stress-response regulatory element
 Patent: JP 199243959-A 12 14-SEP-1999;
 HSP RESEARCH INST INC
 OS Homo sapiens (human)
 PN JP 199243959-A/12
 PD 14-SEP-1999
 PR 04-MAR-1998 JP 1998052453

PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
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Best Local Similarity 52.6%; Pred. No. 1.8e+04;
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Qy 1 CCAATNNNNNNNNCCAGC 19
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Db 1 CCAATGATGTCGACCACG 19
RESULT 11
E28809 19 bp DNA linear PAT 18-JUN-2001
LOCUS Endoplasmic reticulum stress-response regulatory element.
DEFINITION E28809
ACCESSION E28809
VERSION E28809.1 GI:13020863
KEYWORDS JP 1999243959-A/13.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 13 14-SEP-1999;
HSP RESEARCH INST INC
COMMENT OS Mus sp. (mouse)
PN JP 1999243959-A/13
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR
PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
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Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCAGC 19
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Db 1 CCAATGATGTCGACCACG 19
RESULT 12
E44202 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44202
ACCESSION E44202
VERSION E44202.1 GI:18633455
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hideo,Y., Hideki,Y. and Takashi,Y.
TITLE Endoplasmic reticulum stress-response regulatory element
JOURNAL Patent: JP 1999243959-A 13 14-SEP-1999;
HSP RESEARCH INST INC
COMMENT OS Mus sp. (mouse)
PN JP 1999243959-A/13
PD 14-SEP-1999
PF 04-MAR-1998 JP 1998052453
PR
PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT enhancer 1..19.
Location/Qualifiers
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/db_xref="taxon:10095"
BASE COUNT 5 a 6 c 6 g 2 t
ORIGIN

KEYWORDS JP 2001054391-A/1.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 19)
AUTHORS HAJI,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 1 27-FEB-2001;
HSP RESEARCH INST INC
COMMENT OS Artificial Sequence
PN JP 2001054391-A/1
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR
PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09, C12P21/02, C12N15/09, C12R1:91, C12N15/00,
C12N15/00, PC C12R1:91
CC
FH Key Location/Qualifiers
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Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCAGC 19
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Db 1 CCAATNNNNNNNNCCAGC 19
RESULT 13
E44206 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44206
ACCESSION E44206
VERSION E44206.1 GI:18633459
KEYWORDS JP 2001054391-A/5.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS HAJI,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 5 27-FEB-2001;
HSP RESEARCH INST INC
COMMENT OS Homo sapiens (human)
PN JP 2001054391-A/5
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR
PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09, C12P21/02, C12N15/09, C12R1:91, C12N15/00,
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BASE COUNT 3 a 9 c 5 g 2 t
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Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 1 CCAATCGGCGGCTCCACG 19

RESULT 14
E44207 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
ACCESSION E44207
VERSION E44207.1 GI:18633460
KEYWORDS JP 2001054391-A/6.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hagi,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 6 27-FEB-2001;
HSP RESEARCH INST INC

OS Mus sp. (murine)
PN JP 2001054391-A/6
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91))
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FH Key Location/Qualifiers
FT source 1..19
Location/Qualifiers
1..19
/organism="Mus sp. (murine)"
/db_xref="taxon:10095"

BASE COUNT 4 a 8 c 5 g 2 t
ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGGCGGCTCCACG 19

RESULT 15
E44208 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
ACCESSION E44208
VERSION E44208.1 GI:18633461
KEYWORDS JP 2001054391-A/7.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hagi,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 7 27-FEB-2001;
HSP RESEARCH INST INC

OS Rattus sp. (rat)
FT source 1..19
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BASE COUNT 4 a 10 c 4 g 1 t
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QY 1 CCAATNNNNNNNNCCACG 19
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Db 1 CCAATCGGCGGCTCCACG 19

COMMENT

PN JP 2001054391-A/7
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91))
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BASE COUNT 4 a 8 c 5 g 2 t
ORIGIN

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Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 1 CCAATCGGCGGCTCCACG 19

RESULT 16
E44209 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
ACCESSION E44209
VERSION E44209.1 GI:18633462
KEYWORDS JP 2001054391-A/8.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS Hagi,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
TITLE Endoplasmic reticulum stress transcription factor
JOURNAL Patent: JP 2001054391-A 8 27-FEB-2001;
HSP RESEARCH INST INC

OS Homo sapiens (human)
PN JP 2001054391-A/8
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743
PR KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
PC C12N15/09,C12P21/02//((C12N15/09,C12R1:91),C12N15/00,
(C12N15/00, PC C12R1:91))
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FH Key Location/Qualifiers
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Location/Qualifiers
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BASE COUNT 4 a 10 c 4 g 1 t
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Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGGCGGCTCCACG 19

COMMENT

RESULT 17
E44210 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44210
ACCESSION E44210.1 GI:18633463
VERSION JP 2001054391-A/9.
KEYWORDS Gallus sp.
SOURCE
ORGANISM Gallus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 19)
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
Endoplasmic reticulum stress transcription factor
Patent: JP 2001054391-A 9 27-FEB-2001;
HSP RESEARCH INST INC

COMMENT
OS Gallus sp. (chicken)
PN JP 2001054391-A/9
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743

REFERENCE
AUTHORS
TITLE
JOURNAL

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/db_xref="taxon:9036"

BASE COUNT 5 a 7 c 6 g 1 t

ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 1 CCAATGGAGCGCCACCAG 19

RESULT 18
E44211 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44211
ACCESSION E44211.1 GI:18633464
VERSION JP 2001054391-A/10.
KEYWORDS Homo sapiens.
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 19)
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
Endoplasmic reticulum stress transcription factor
Patent: JP 2001054391-A 10 27-FEB-2001;
HSP RESEARCH INST INC

COMMENT
OS Homo sapiens (human)
PN JP 2001054391-A/10
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743

REFERENCE
AUTHORS
TITLE
JOURNAL

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source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 6 a 6 c 6 g 1 t

ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGAGCGCGCCACG 19

RESULT 20
E44213 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44213
ACCESSION E44213.1 GI:18633466
VERSION JP 2001054391-A/12.
KEYWORDS Homo sapiens.
SOURCE
ORGANISM Homo sapiens

FT source 1..19
/organism="Homo sapiens (human)".
FT Location/Qualifiers
source 1..19
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 6 a 6 c 6 g 1 t

ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
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Db 1 CCAATCGAGCGCGCCACG 19

RESULT 19
E44212 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44212
ACCESSION E44212.1 GI:18633465
VERSION JP 2001054391-A/11.
KEYWORDS Gallus sp.
SOURCE
ORGANISM Gallus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 19)
Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
Endoplasmic reticulum stress transcription factor
Patent: JP 2001054391-A 11 27-FEB-2001;
HSP RESEARCH INST INC

COMMENT
OS Gallus sp. (chicken)
PN JP 2001054391-A/11
PD 27-FEB-2001
PF 11-NOV-1999 JP 1999321743

REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES
source Location/Qualifiers
FT 1..19
FT source /organism="Gallus sp. (chicken)".
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/organism="Gallus sp."
/db_xref="taxon:9036"

BASE COUNT 4 a 9 c 5 g 1 t

ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
||||| |||||
Db 1 CCAATCGAGCGCGCCACG 19

RESULT 20
E44213 19 bp DNA linear PAT 31-JAN-2002
LOCUS Endoplasmic reticulum stress transcription factor.
DEFINITION E44213
ACCESSION E44213.1 GI:18633466
VERSION JP 2001054391-A/12.
KEYWORDS Homo sapiens.
SOURCE
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 AUTHORS Hajj, K., Yoshida, H., Mori, K., Yanaqi, H. and Yura, T.
 TITLE Endoplasmic reticulum stress transcription factor
 JOURNAL Patent: JP 2001054391-A 12 27-FEB-2001;
 HSP RESEARCH INST INC

COMMENT OS Homo sapiens (human)
 PN JP 2001054391-A/12
 PD 27-FEB-2001
 PF 11-NOV-1999 JP 1999321743

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 TAKASHI YURA
 PC C12N15/09, C12P21/02//((C12N15/09, C12R1:91), C12N15/00,
 (C12N15/00, PC C12R1:91)
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 FT source 1..19 /organism='Homo sapiens (human)'

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 ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
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 Db 1 CCAATGATGTCGACCACG 19

RESULT 21
 E44214 LOCUS E44214 19 bp DNA linear PAT 31-JAN-2002
 DEFINITION Endoplasmic reticulum stress transcription factor.
 ACCESSION E44214
 VERSION E44214.1 GI:18633467
 KEYWORDS JP 2001054391-A/13.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 AUTHORS Hajj, K., Yoshida, H., Mori, K., Yanaqi, H. and Yura, T.
 TITLE Endoplasmic reticulum stress transcription factor
 JOURNAL Patent: JP 2001054391-A 13 27-FEB-2001;
 HSP RESEARCH INST INC

COMMENT OS Mus sp. (murine)
 PN JP 2001054391-A/13
 PD 27-FEB-2001
 PF 11-NOV-1999 JP 1999321743

PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
 TAKASHI YURA
 PC C12N15/09, C12P21/02//((C12N15/09, C12R1:91), C12N15/00,
 (C12N15/00, PC C12R1:91)
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 FH key Location/Qualifiers
 FT source 1..19 /organism='Mus sp. (murine)'

FEATURES
 source Location/Qualifiers
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 /db_xref='taxon:10095'
 BASE COUNT 5 a 6 c 6 g 2 t
 ORIGIN

Query Match 52.6%; Score 10; DB 6; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
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 Db 1 CCAATGATGTCGACCACG 19

RESULT 22
 AX443752/c LOCUS AX443752 24 bp DNA linear PAT 03-JUL-2002
 DEFINITION Sequence 207 from Patent WO0216649.
 ACCESSION AX443752
 VERSION AX443752.1 GI:21691030
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1
 AUTHORS Gunderson, K.
 TITLE Probes and decoder oligonucleotides
 JOURNAL Patent: WO 0216649-A 207 28-FEB-2002;
 Illumina, Inc. (US)

FEATURES
 source Location/Qualifiers
 1..24 /organism='synthetic construct'
 /db_xref='taxon:32630'
 /note='Computer Generated Probe Sequence.'

BASE COUNT 4 a 5 c 9 g 6 t
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 Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
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 Db 23 CCAATATTACGTGACCACG 5

RESULT 23
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 DEFINITION Sequence 4188 from Patent WO0216649.
 ACCESSION AX447733
 VERSION AX447733.1 GI:21696632
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1
 AUTHORS Gunderson, K.
 TITLE Probes and decoder oligonucleotides
 JOURNAL Patent: WO 0216649-A 4188 28-FEB-2002;
 Illumina, Inc. (US)

FEATURES
 source Location/Qualifiers
 1..25 /organism='synthetic construct'
 /db_xref='taxon:32630'
 /note='Computer Generated Probe Sequence.'

BASE COUNT 4 a 5 c 9 g 7 t
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 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
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 Db 24 CCAATATTACGTGACCACG 6

RESULT 24


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VERSION      AX343726.1  GI:18491804
KEYWORDS
SOURCE
ORGANISM      Pseudacanthotermes spiniger
REFERENCE
AUTHORS      Lambert, M., Bulet, P., Latorse, M.P. and Hoffmann, J.
TITLE        Antimicrobial peptides of the family of defensins, polynucleotides
              encoding said peptides, transformed vectors and organisms
              containing them
              Patent: WO 0200706-A 1 03-JAN-2002;
              Rhobio (FR)
FEATURES
  source      Location/Qualifiers
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Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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LOCUS      E28800      122 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Endoplasmic reticulum stress-response regulatory element.
ACCESSION   E28800
VERSION     1
KEYWORDS    GI:13020854
SOURCE      JP 1999243959-A/4.
ORGANISM    Homo sapiens.
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 122)
AUTHORS    Hideo, Y., Hideki, T. and Takashi, Y.
TITLE      Endoplasmic reticulum stress-response regulatory element
JOURNAL    HSP RESEARCH INST INC
            Patent: JP 1999243959-A 4 14-SEP-1999;
COMMENT     OS Homo sapiens (human)
            PN JP 1999243959-A/4
            PD 14-SEP-1999
            PF 04-MAR-1998 JP 1998052453
            PR
            PI HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
            PC C12N15/09, A61K35/74, A61K38/00, A61K48/00, C12N15/00,
            CC Strandedness: Double;
            CC Topology: Linear;
            FH Key
            FT enhancer 15..33
            FT enhancer 47..65
            FT enhancer 80..98
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            Location/Qualifiers
              1..122
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
BASE COUNT    22 a 35 c 48 g 17 t
ORIGIN

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Query Match    52.6%; Score 10; DB 6; Length 122;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
Db 80 CCAATCGCGCGCTCCACG 98
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LOCUS      E44205      122 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Endoplasmic reticulum stress transcription factor.
ACCESSION   E44205
VERSION     1
KEYWORDS    GI:18633458
SOURCE      JP 2001054391-A/4.
ORGANISM    Homo sapiens.
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 122)
AUTHORS    Hajji, K., Yoshida, H., Mori, K., Yanagi, H. and Yura, T.
TITLE      Endoplasmic reticulum stress transcription factor
JOURNAL    HSP RESEARCH INST INC
            Patent: JP 2001054391-A 4 27-FEB-2001;
COMMENT     OS Homo sapiens (human)
            PN JP 2001054391-A/4
            PD 27-FEB-2001
            PF 11-NOV-1999 JP 1999321743
            PR
            PI KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
            TAKASHI YURA
            PC C12N15/09, C12P21/02, C12N15/09, C12R1:91, C12N15/00,
            CC (C12N15/00, PC C12R1:91)
            CC
            FH Key
            FT source 1..122
            Location/Qualifiers
              1..122
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
BASE COUNT    22 a 35 c 48 g 17 t
ORIGIN
Query Match    52.6%; Score 10; DB 6; Length 122;
Best Local Similarity 52.6%; Pred. No. 1.8e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 1 CCAATNNNNNNNNCCACG 19
Db 80 CCAATCGCGCGCTCCACG 98
E271990
LOCUS      E271990/c      125 bp      DNA      linear      VRL 02-JUN-2001
DEFINITION Human adenovirus type 19p strain 587 inverted terminal repeat,
              partial sequence.
ACCESSION   AF271990
VERSION     1
KEYWORDS    GI:14279590
SOURCE      AF271990.1
ORGANISM    human adenovirus type 19p.
              human adenovirus type 19p.
              Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
              1 (bases 1 to 125)
REFERENCE   Blusch, J.H., Deryckere, F., Windheim, M., Ruzsics, Z., Arberg, N.,
              Adriaen, T. and Burgerlt, H.G.
              E3/49K: A Novel Early Region 3 Protein Specifically Expressed By
              Adenoviruses of Subgroup D
              Unpublished
              2 (bases 1 to 125)
JOURNAL
REFERENCE

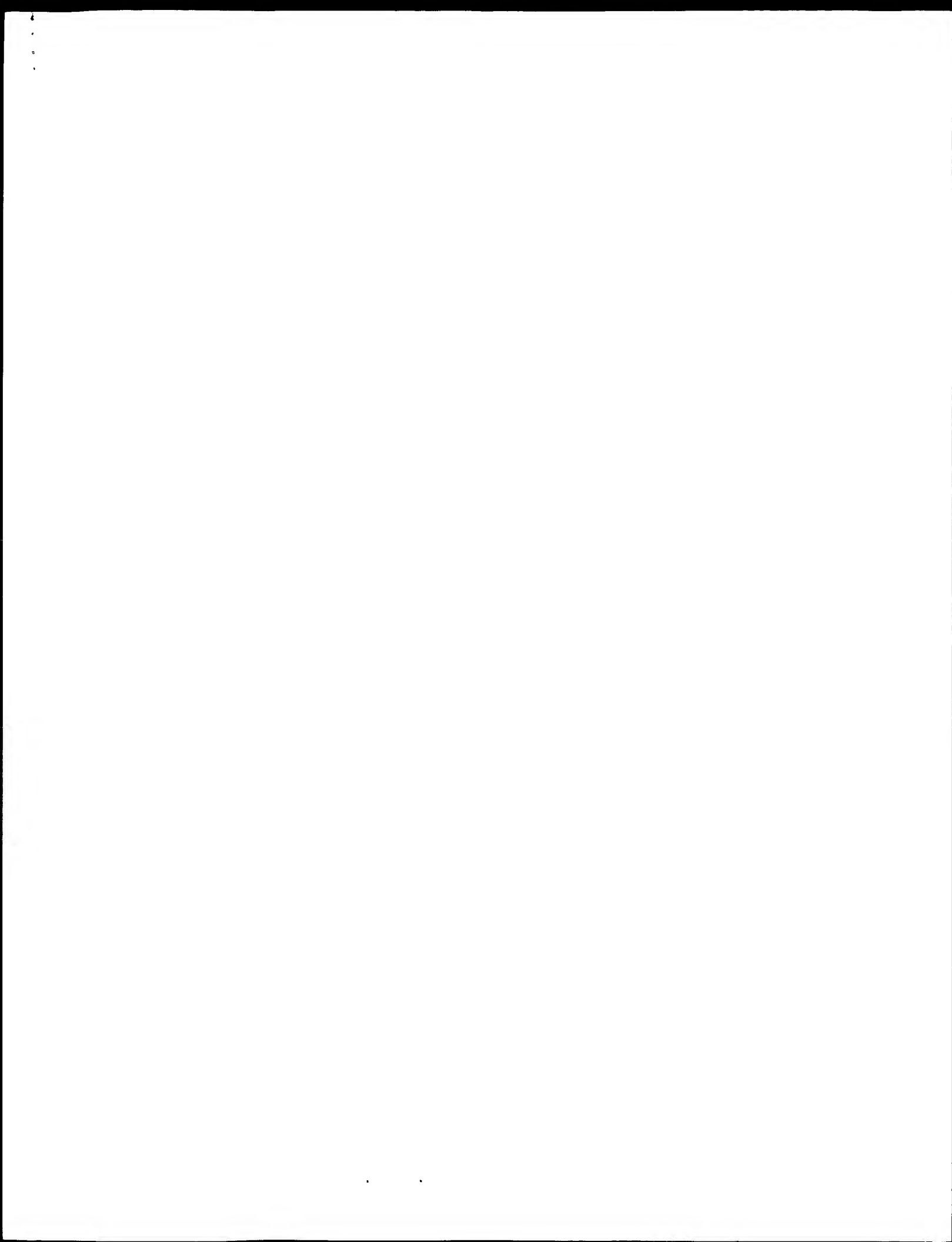
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AUTHORS Ruzsics, Z. and Burgert, H.G.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAY-2000) Dep. of Virology, Gene Center-Max V.
 Pettenkofer Inst., Feodor-Lynen-Str. 25, Muenchen 81377, Germany

FEATURES
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 /strain="587"
 /serotype="19p"
 /specific_host="Homo sapiens"
 /db_xref="taxon:134640"
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 BASE COUNT 43 a 25 c 28 g 29 t
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 Best Local Similarity 52.6%; Pred. No. 1.8e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCAATNNNNNNNNCCACG 19
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 Db 86 CCAATCAACGACGACCACG 68

Search completed: November 16, 2002, 02:59:16
 Job time : 2579 secs



Mon Nov 18 08:09:24 2002

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: November 16, 2002, 01:16:17 : Search time 257 Seconds
(without alignments)
166.490 Million cell updates/sec

Title: US-09-606-804-1
Perfect score: 19
Sequence: 1 ccaatnnnnnnccacg 19
Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues
Total number of hits satisfying chosen parameters: 4370478
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 90 summaries

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SUMMARIES

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	52.6	19	20	AA225631	Endoplasmic reticu
2	52.6	19	20	AA225632	Endoplasmic reticu
3	52.6	19	20	AA225633	Endoplasmic reticu
4	52.6	19	20	AA225634	Endoplasmic reticu
5	52.6	19	20	AA225635	Endoplasmic reticu
6	52.6	19	20	AA225636	Endoplasmic reticu
7	52.6	19	20	AA225637	Endoplasmic reticu
8	52.6	19	20	AA225638	Endoplasmic reticu
9	52.6	19	20	AA225639	Endoplasmic reticu

10	52.6	19	20	AA225640	Endoplasmic reticu
11	52.6	19	21	AAA28570	GRP78 promoter ERS
12	52.6	19	21	AAA28571	GRP78 promoter ERS
13	52.6	19	21	AAA28572	GRP78 promoter ERS
14	52.6	19	21	AAA28573	GRP78 promoter ERS
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16	52.6	19	21	AAA28575	GRP78 promoter ERS
17	52.6	19	21	AAA28576	GRP78 promoter ERS
18	52.6	19	21	AAA28577	GRP78 promoter ERS
19	52.6	19	21	AAA28578	GRP78 promoter ERS
20	52.6	19	21	AAA28579	GRP78 promoter ERS
21	52.6	19	21	AAA28580	GRP78 promoter ERS
22	52.6	19	21	AAA28581	GRP78 promoter ERS
23	52.6	19	21	AAA28582	GRP78 promoter ERS
24	52.6	19	21	AAA28583	GRP78 promoter ERS
25	52.6	19	21	AAA28584	GRP78 promoter ERS
26	52.6	19	21	AAA28585	GRP78 promoter ERS
27	52.6	19	21	AAA28586	GRP78 promoter ERS
28	52.6	19	21	AAA28587	GRP78 promoter ERS
29	52.6	19	21	AAA28588	GRP78 promoter ERS
30	52.6	19	21	AAA28589	GRP78 promoter ERS
31	52.6	19	21	AAA28590	GRP78 promoter ERS
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33	52.6	19	21	AAA28592	GRP78 promoter ERS
34	52.6	19	21	AAA28593	GRP78 promoter ERS
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39	52.6	19	21	AAA28598	GRP78 promoter ERS
40	52.6	19	21	AAA28599	GRP78 promoter ERS
41	52.6	19	21	AAA28600	GRP78 promoter ERS
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45	52.6	19	21	AAA28604	GRP78 promoter ERS
46	52.6	19	21	AAA28605	GRP78 promoter ERS
47	52.6	19	21	AAA28606	GRP78 promoter ERS
48	52.6	19	21	AAA28607	GRP78 promoter ERS
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51	52.6	19	21	AAA28610	GRP78 promoter ERS
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54	52.6	19	21	AAA28613	GRP78 promoter ERS
55	52.6	19	21	AAA28614	GRP78 promoter ERS
56	52.6	19	21	AAA28615	GRP78 promoter ERS
57	52.6	19	21	AAA28616	GRP78 promoter ERS
58	52.6	19	21	AAA28617	GRP78 promoter ERS
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60	52.6	19	21	AAA28619	GRP78 promoter ERS
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63	52.6	19	21	AAA28622	GRP78 promoter ERS
64	52.6	19	21	AAA28623	GRP78 promoter ERS
65	52.6	19	21	AAA28624	GRP78 promoter ERS
66	52.6	19	21	AAA28625	GRP78 promoter ERS
67	52.6	19	21	AAA28626	GRP78 promoter ERS
68	52.6	19	21	AAA28627	GRP78 promoter ERS
69	52.6	19	21	AAA28628	GRP78 promoter ERS
70	52.6	19	21	AAA28629	GRP78 promoter ERS
71	52.6	19	21	AAA28630	GRP78 promoter ERS
72	52.6	19	21	AAA28631	GRP78 promoter ERS
73	52.6	19	21	AAA28632	GRP78 promoter ERS
74	52.6	19	21	AAA28633	GRP78 promoter ERS
75	52.6	19	21	AAA28634	GRP78 promoter ERS
76	52.6	19	21	AAA28635	GRP78 promoter ERS
77	52.6	19	21	AAA28636	GRP78 promoter ERS
78	52.6	19	21	AAA28637	GRP78 promoter ERS
79	52.6	19	21	AAA28638	GRP78 promoter ERS
80	52.6	19	21	AAA28639	GRP78 promoter ERS
81	52.6	19	21	AAA28640	GRP78 promoter ERS
82	52.6	19	21	AAA28641	GRP78 promoter ERS

[illegible]

XX Example 1: Fig 3; 25pp; Japanese.

PS The present invention specifically claims an element shown by: (A) a

XX 19 bp base sequence, CCAATNNNN NNNCCAGC (ERSE); or (B) a modified base

CC sequence having replaced 1-3 bases with the other base(s), which induces

CC transcription with stress on endoplasmic reticulum used for stress

CC competence of endoplasmic reticulum. Also described are: (1) a DNA

CC having transcription inducing activity with stress on endoplasmic

CC reticulum containing the above mentioned element, optionally further

CC optionally with the DNA. The element can be used for the inhibition of

CC growth and induction of apoptosis of cancer cells, and improvement of

CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of

CC autoantibody formation. AA225632 to AA225657 represent elements used in

CC an example from the present invention.

XX

Sequence 19 BP: 4 A; 8 C; 5 G; 2 T; 0 other;

XX

Query Match 52.6%; Score 10; DB 20; Length 19;

Best Local Similarity 52.6%; Pred. No. 1,4e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0

Oy 1 CCAATNNNNNNNNCCAGC 19

1 |||||

1 CCAATCGAGCGCTCCAGC 19

Db

RESULT 5

AA225635

ID AA225635 standard: DNA: 19 BP.

XX

AC AA225635;

XX

DT 23-DEC-1999 (first entry)

XX

DE Endoplasmic reticulum stress competence control element SEQ ID NO:8.

XX

KW Endoplasmic reticulum; ER; stress competence; control element;

XX inhibition; growth; apoptosis; cancer; autoimmune disease;

XX cystic fibrosis; ds.

XX

OS Homo sapiens.

XX

PN JP11243959-A.

XX

PD 14-SEP-1999.

XX

PF 04-MAR-1998; 98JP-0052453.

XX

PR 04-MAR-1998; 98JP-0052453.

XX

PA (HSPK-) HSP KENKYUSHO KK.

XX

DR WPI: 1999-603708/52.

XX

PT New control element for stress competence of endoplasmic reticulum -

PT useful for inhibition of growth and induction of apoptosis in cancer

PT cells

XX

PS Example 1: Fig 3; 25pp; Japanese.

XX

The present invention specifically claims an element shown by: (A) a

CC 19 bp base sequence, CCAATNNNN NNNCCAGC (ERSE); or (B) a modified base

CC sequence having replaced 1-3 bases with the other base(s), which induces

CC transcription with stress on endoplasmic reticulum used for stress

CC competence of endoplasmic reticulum. Also described are: (1) a DNA

CC having transcription inducing activity with stress on endoplasmic

CC reticulum containing the above mentioned element, optionally further

CC optionally with the DNA; and (2) a vector containing the element

CC containing a promoter DNA; and (3) a vector containing the element

CC optionally with the DNA. The element can be used for the inhibition of

CC growth and induction of apoptosis of cancer cells, and improvement of

CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of

CC

CC autoantibody formation. AA25632 to AA25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 1 CCAATCGCGCCGACCACG 19
|||||
RESULT 6
AA25636
ID AA25636 standard; DNA; 19 BP.
XX
AC AA25636;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:9.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
OS Gallus sp.
XX
PN JP11243959-A.
XX
PD 14-SEP-1999.
XX
PF 04-MAR-1998; 98JP-0052453.
XX
PR 04-MAR-1998; 98JP-0052453.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
WP; 1999-603708/52.
XX
DR
XX
PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNNNNNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AA25632 to AA25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 1 CCAATGGAGCGCACCACG 19
|||||

RESULT 7
AA25637
ID AA25637 standard; DNA; 19 BP.
XX
AC AA25637;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:10.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX
OS Homo sapiens.
XX
PN JP11243959-A.
XX
PD 14-SEP-1999.
XX
PF 04-MAR-1998; 98JP-0052453.
XX
PR 04-MAR-1998; 98JP-0052453.
XX
PA (HSPK-) HSP KENKYUSHO KK.
XX
WP; 1999-603708/52.
XX
DR
XX
PT New control element for stress competence of endoplasmic reticulum -
PT useful for inhibition of growth and induction of apoptosis in cancer
PT cells
XX
PS Example 1; Fig 3; 25pp; Japanese.
XX
CC The present invention specifically claims an element shown by: (A) a
CC 19 bp base sequence, CCAATNNNNNNNNCCACG (ERSE); or (B) a modified base
CC sequence having replaced 1-3 bases with the other base(s), which induces
CC transcription with stress on endoplasmic reticulum used for stress
CC competence of endoplasmic reticulum. Also described are: (1) a DNA
CC having transcription inducing activity with stress on endoplasmic
CC reticulum containing the above mentioned element, optionally further
CC containing a promoter DNA; and (2) a vector containing the element
CC optionally with the DNA. The element can be used for the inhibition of
CC growth and induction of apoptosis of cancer cells, and improvement of
CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
CC autoantibody formation. AA25632 to AA25657 represent elements used in
CC an example from the present invention.
XX
SQ Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 other;
Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 1 CCAATCGCAAGGACCACG 19
|||||
RESULT 8
AA25638
ID AA25638 standard; DNA; 19 BP.
XX
AC AA25638;
XX
DT 23-DEC-1999 (first entry)
XX
DE Endoplasmic reticulum stress competence control element SEQ ID NO:11.
XX
KW Endoplasmic reticulum; ER; stress competence; control element;
KW inhibition; growth; apoptosis; cancer; autoimmune disease;
KW cystic fibrosis; ds.
XX

OS Gallus sp.
 XX JP11243959-A.
 PN 14-SEP-1999.
 PD 04-MAR-1998: 98JP-0052453.
 PF 04-MAR-1998: 98JP-0052453.
 PR 04-MAR-1998: 98JP-0052453.
 XX (HSPK-) HSP KENKYUSHO KK.
 PA WPI: 1999-603708/52.
 DR
 XX
 PT New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer
 cells
 PS
 PS Example 1: Fig 3: 25pp: Japanese.
 CC The present invention specifically claims an element shown by: (A) a
 CC 19 bp base sequence, CCAATNNNNN NNNCCAG (ERSE); or (B) a modified base
 CC sequence having replaced 1-3 bases with the other base(s), which induces
 CC transcription with stress on endoplasmic reticulum. Also described are: (1) a DNA
 CC having transcription inducing activity with stress on endoplasmic
 CC reticulum containing the above mentioned element, optionally further
 CC containing a promoter DNA; and (2) a vector containing the element
 CC optionally with the DNA. The element can be used for the inhibition of
 CC growth and induction of apoptosis of cancer cells, and improvement of
 CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
 CC autoantibody formation. AA25632 to AA25657 represent elements used in
 CC an example from the present invention.
 CC
 SQ Sequence 19 BP: 4 A; 9 C; 5 G; 1 T; 0 other:
 Query Match 52.6%; Score 10; DB 20; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.4e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 1 CCAATNNNNNNNNCCAG 19
 |||||
 DB 1 CCAATGCAGCGCGCCAGC 19
 |||||
 RESULT 9
 AA25639
 ID AA25639 standard; DNA: 19 BP.
 AC AA25639;
 XX
 DT 23-DEC-1999 (first entry)
 DT
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:12.
 XX
 KW Endoplasmic reticulum; ER; stress competence; control element;
 KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX
 OS Homo sapiens.
 XX
 PN JP11243959-A.
 PN 14-SEP-1999.
 PD 04-MAR-1998: 98JP-0052453.
 PF 04-MAR-1998: 98JP-0052453.
 PR 04-MAR-1998: 98JP-0052453.
 XX (HSPK-) HSP KENKYUSHO KK.
 PA WPI: 1999-603708/52.
 DR
 XX

PT New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer
 cells
 PS
 PS Example 1: Fig 3: 25pp: Japanese.
 CC The present invention specifically claims an element shown by: (A) a
 CC 19 bp base sequence, CCAATNNNNN NNNCCAG (ERSE); or (B) a modified base
 CC sequence having replaced 1-3 bases with the other base(s), which induces
 CC transcription with stress on endoplasmic reticulum. Also described are: (1) a DNA
 CC having transcription inducing activity with stress on endoplasmic
 CC reticulum containing the above mentioned element, optionally further
 CC containing a promoter DNA; and (2) a vector containing the element
 CC optionally with the DNA. The element can be used for the inhibition of
 CC growth and induction of apoptosis of cancer cells, and improvement of
 CC symptoms of autoimmune diseases and cystic fibrosis by inhibition of
 CC autoantibody formation. AA25632 to AA25657 represent elements used in
 CC an example from the present invention.
 CC
 SQ Sequence 19 BP: 5 A; 6 C; 5 G; 3 T; 0 other:
 Query Match 52.6%; Score 10; DB 20; Length 19;
 Best Local Similarity 52.6%; Pred. No. 1.4e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 OY 1 CCAATNNNNNNNNCCAG 19
 |||||
 DB 1 CCAATGATGTCGACCCAGC 19
 |||||
 RESULT 10
 AA25640
 ID AA25640 standard; DNA: 19 BP.
 AC AA25640;
 XX
 DT 23-DEC-1999 (first entry)
 DT
 DE Endoplasmic reticulum stress competence control element SEQ ID NO:13.
 XX
 KW Endoplasmic reticulum; ER; stress competence; control element;
 KW inhibition; growth; apoptosis; cancer; autoimmune disease;
 KW cystic fibrosis; ds.
 XX
 OS Mus sp.
 XX
 PN JP11243959-A.
 PN 14-SEP-1999.
 PD 04-MAR-1998: 98JP-0052453.
 PF 04-MAR-1998: 98JP-0052453.
 PR 04-MAR-1998: 98JP-0052453.
 XX (HSPK-) HSP KENKYUSHO KK.
 PA WPI: 1999-603708/52.
 DR
 XX
 PT New control element for stress competence of endoplasmic reticulum -
 PT useful for inhibition of growth and induction of apoptosis in cancer
 cells
 PS
 PS Example 1: Fig 3: 25pp: Japanese.
 CC The present invention specifically claims an element shown by: (A) a
 CC 19 bp base sequence, CCAATNNNNN NNNCCAG (ERSE); or (B) a modified base
 CC sequence having replaced 1-3 bases with the other base(s), which induces
 CC transcription with stress on endoplasmic reticulum. Also described are: (1) a DNA
 CC having transcription inducing activity with stress on endoplasmic
 CC reticulum containing the above mentioned element, optionally further
 CC containing a promoter DNA; and (2) a vector containing the element

optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AA225632 to AA225651 represent elements used in an example from the present invention.

Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other:

Query Match 52.6%; Score 10; DB 20; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 CCAATNNNNNNNNCCAGC 19
1 CCAATGAGCGCTCCAGCAGC 19

RESULT 11
AAA28570

ID AAA28570 standard; DNA: 19 BP.

AC AAA28570;

DT 29-AUG-2000 (first entry)

DE GRP78 promoter ERSE1-like sequence.

Endoplasmic reticulum; stress; ER; transcription factor;
transcription; regulatory element; ERSE; bZIP; chaperone; treatment;

propylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;

gene expression; GRP; glucose regulated protein; promoter; ss.

Homo sapiens.

WO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI: 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)
for controlling expression of endoplasmic reticulum chaperone, useful
for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)
capable of regulating transcription inducing activity exhibited by an
element (ERSE) can be used in a method for controlling expression of
an endoplasmic reticulum chaperone. The method comprises expressing
bZIP. The method can be used for expression of a foreign protein by
positively regulating expression of an endoplasmic reticulum
chaperone gene. bZIP is useful for controlling the expression of
endoplasmic reticulum chaperone either positively or negatively in
cells and therefore is useful for treatment or prophylaxis of
cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
wounds and ulcers. bZIP also maintains the correct conformation of
the endoplasmic reticulum chaperone and thereby increases the
expression of a foreign protein. This sequence taken from the
glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
sequence.

Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other:

Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 CCAATNNNNNNNNCCAGC 19
1 CCAATCGCGCTCCAGCAGC 19

RESULT 12

AAA28571

ID AAA28571 standard; DNA: 19 BP.

AC AAA28571;

DT 29-AUG-2000 (first entry)

DE GRP78 promoter ERSE1-like sequence.

Endoplasmic reticulum; stress; ER; transcription factor;
transcription; regulatory element; ERSE; bZIP; chaperone; treatment;

propylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;

gene expression; GRP; glucose regulated protein; promoter; ss.

Mus musculus.

WO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI: 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)
for controlling expression of endoplasmic reticulum chaperone, useful
for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)
capable of regulating transcription inducing activity exhibited by an
element (ERSE) can be used in a method for controlling expression of
an endoplasmic reticulum chaperone. The method comprises expressing
bZIP. The method can be used for expression of a foreign protein by
positively regulating expression of an endoplasmic reticulum
chaperone gene. bZIP is useful for controlling the expression of
endoplasmic reticulum chaperone either positively or negatively in
cells and therefore is useful for treatment or prophylaxis of
cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
wounds and ulcers. bZIP also maintains the correct conformation of
the endoplasmic reticulum chaperone and thereby increases the
expression of a foreign protein. This sequence taken from the
glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
sequence.

Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other:

Query Match 52.6%; Score 10; DB 21; Length 19;
Best Local Similarity 52.6%; Pred. No. 1.4e+03;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 |||||
 DB 1 CCAATCGAGCGCTCCACG 19

RESULT 13

AAA28572 standard; DNA: 19 BP.

AAA28572:

29-AUG-2000 (first entry)

GRP78 promoter ERSE1-like sequence.

Endoplasmic reticulum stress; ER: transcription factor;
 transcription: regulatory element; ERSE: bZIP; chaperone; treatment;
 prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
 cystic fibrosis; ulcer; gene therapy; recombinant gene; rat;
 gene expression; GRP; glucose regulated protein; promoter; ss.

Rattus rattus.

MO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI: 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)
 for controlling expression of endoplasmic reticulum chaperone, useful
 for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)
 capable of regulating transcription inducing actively exhibited by an
 element (ERSE) can be used in a method for controlling expression of
 an endoplasmic reticulum chaperone. The method comprises expressing
 bZIP. The method can be used for expression of a foreign protein by
 positively regulating expression of an endoplasmic reticulum
 chaperone gene. bZIP is useful for controlling the expression of
 endoplasmic reticulum chaperone either positively or negatively in
 cells and therefore is useful for treatment or prophylaxis of
 cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 wounds and ulcers. bZIP also maintains the correct conformation of
 the endoplasmic reticulum chaperone and thereby increases the
 expression of a foreign protein. This sequence taken from the
 glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
 sequence.

Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other:

Query Match 52.6%; Score 10; DB 21; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.4e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 |||||
 DB 1 CCAATCGAGCGCTCCACG 19

RESULT 14

AAA28573 standard; DNA: 19 BP.

AAA28573:

29-AUG-2000 (first entry)

GRP94 promoter ERSE1-like sequence.

Endoplasmic reticulum stress; ER: transcription factor;
 transcription: regulatory element; ERSE: bZIP; chaperone; treatment;
 prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
 cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
 gene expression; GRP; glucose regulated protein; promoter; ss.

Homo sapiens.

MO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI: 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)
 for controlling expression of endoplasmic reticulum chaperone, useful
 for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
 diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)
 capable of regulating transcription inducing actively exhibited by an
 element (ERSE) can be used in a method for controlling expression of
 an endoplasmic reticulum chaperone. The method comprises expressing
 bZIP. The method can be used for expression of a foreign protein by
 positively regulating expression of an endoplasmic reticulum
 chaperone gene. bZIP is useful for controlling the expression of
 endoplasmic reticulum chaperone either positively or negatively in
 cells and therefore is useful for treatment or prophylaxis of
 cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 wounds and ulcers. bZIP also maintains the correct conformation of
 the endoplasmic reticulum chaperone and thereby increases the
 expression of a foreign protein. This sequence taken from the
 glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
 sequence.

Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other:

Query Match 52.6%; Score 10; DB 21; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.4e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 |||||

DB 1 CCAATCGAGCGCTCCACG 19

RESULT 15

AAA28574 standard; DNA: 19 BP.

AAA28574:

29-AUG-2000 (first entry)

XX GRP94 promoter ERSE1-like sequence.

DE Endoplasmic reticulum; stress; ER; transcription factor;
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 KW prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
 KW cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken;
 KW gene expression; GRP; glucose regulated protein; promoter; ss.
 OS Gallus domesticus.

WO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI; 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (bZIP)
 CC capable of regulating transcription inducing activity exhibited by an
 CC element (ERSE) can be used in a method for controlling expression of
 CC an endoplasmic reticulum chaperone. The method comprises expressing
 CC bZIP. The method can be used for expression of a foreign protein by
 CC positively regulating expression of an endoplasmic reticulum
 CC chaperone gene. bZIP is useful for controlling the expression of
 CC endoplasmic reticulum chaperone either positively or negatively in
 CC cells and therefore is useful for treatment or prophylaxis of
 CC cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 CC wounds and ulcers. bZIP also maintains the correct conformation of
 CC the endoplasmic reticulum chaperone and thereby increases the
 CC expression of a foreign protein. This sequence taken from the
 CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
 CC sequence.

SO Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;

Query Match

Best Local Similarity 52.6%; Score 10; DB 21; Length 19;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19

DB 1 CCAATGGAGCGCACACG 19

RESULT 16

AAA28575

ID AAA28575 standard; DNA; 19 BP.

AC AAA28575;

29-AUG-2000 (first entry)

GRP94 promoter ERSE3-like sequence.

Endoplasmic reticulum; stress; ER; transcription factor;
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 KW prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;

KW cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
 KW gene expression; GRP; glucose regulated protein; promoter; ss.
 OS Homo sapiens.

WO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99WO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI; 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic diseases, wounds and ulcers

Example 1; Fig 3; 157pp; English.

XX An endoplasmic reticulum stress transcription factor (bZIP)
 CC capable of regulating transcription inducing activity exhibited by an
 CC element (ERSE) can be used in a method for controlling expression of
 CC an endoplasmic reticulum chaperone. The method comprises expressing
 CC bZIP. The method can be used for expression of a foreign protein by
 CC positively regulating expression of an endoplasmic reticulum
 CC chaperone gene. bZIP is useful for controlling the expression of
 CC endoplasmic reticulum chaperone either positively or negatively in
 CC cells and therefore is useful for treatment or prophylaxis of
 CC cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 CC wounds and ulcers. bZIP also maintains the correct conformation of
 CC the endoplasmic reticulum chaperone and thereby increases the
 CC expression of a foreign protein. This sequence taken from the
 CC glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
 CC sequence.

SO Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 other;

Query Match

Best Local Similarity 52.6%; Score 10; DB 21; Length 19;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19

DB 1 CCAATGGAGCGCACACG 19

RESULT 17

AAA28576

ID AAA28576 standard; DNA; 19 BP.

AC AAA28576;

29-AUG-2000 (first entry)

GRP94 promoter ERSE3-like sequence.

Endoplasmic reticulum; stress; ER; transcription factor;
 KW transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
 KW prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
 KW cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken;
 KW gene expression; GRP; glucose regulated protein; promoter; ss.
 OS Gallus domesticus.

WO200029429-A2.


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XX 25-MAY-2000.
XX
XX 12-NOV-1999; 99WO-JP06305.
XX
XX 13-NOV-1998; 98JP-0324227.
PR 09-JUN-1999; 99JP-0163112.
XX
XX (HSPR-) HSP RES INST INC.
XX
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX
XX WPI: 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
XX for controlling expression of endoplasmic reticulum chaperone, useful
XX for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
XX diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
XX capable of regulating transcription inducing activity exhibited by an
XX element (ERSE) can be used in a method for controlling expression of
XX an endoplasmic reticulum chaperone. The method comprises expressing
XX bZIP. The method can be used for expression of a foreign protein by
XX positively regulating expression of an endoplasmic reticulum
XX chaperone gene. bZIP is useful for controlling the expression of
XX endoplasmic reticulum chaperone either positively or negatively in
XX cells and therefore is useful for treatment or prophylaxis of
XX cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
XX wounds and ulcers. bZIP also maintains the correct conformation of
XX the endoplasmic reticulum chaperone and thereby increases the
XX expression of a foreign protein. This sequence taken from the
XX glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
XX sequence.
XX
XX Sequence 19 BP; 4 A; 9 C; 5 G; 1 T; 0 other:
XX
XX Query Match 52.6%; Score 10; DB 21; Length 19;
XX Best Local Similarity 52.6%; Pred. No. 1.4e+03;
XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 CCAATNNNNNNNNCCACG 19
XX 1 CCAATGACGCGCCACG 19
XX
XX Db
XX
XX RESULT 18
XX AAA28577
XX ID AAA28577 standard; DNA; 19 BP.
XX
XX AC AAA28577;
XX
XX DT 29-AUG-2000 (first entry)
XX
XX DE Calreticulin promoter ERSE3-like sequence.
XX
XX KM Endoplasmic reticulum stress; ER; transcription factor;
XX transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
XX prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
XX cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
XX gene expression; GRP; glucose regulated protein; promoter; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200029429-A2.
XX
XX PD 25-MAY-2000.
XX
XX PF 12-NOV-1999; 99WO-JP06305.
XX
XX PR 13-NOV-1998; 98JP-0324227.
XX
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PR 09-JUN-1999; 99JP-0163112.
XX
XX (HSPR-) HSP RES INST INC.
XX
XX Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX
XX WPI: 2000-387736/33.
XX
XX New endoplasmic reticulum stress transcription factor (known as bZIP)
XX for controlling expression of endoplasmic reticulum chaperone, useful
XX for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
XX diseases, wounds and ulcers
XX
XX Example 1; Fig 3; 157pp; English.
XX
XX An endoplasmic reticulum stress transcription factor (bZIP)
XX capable of regulating transcription inducing activity exhibited by an
XX element (ERSE) can be used in a method for controlling expression of
XX an endoplasmic reticulum chaperone. The method comprises expressing
XX bZIP. The method can be used for expression of a foreign protein by
XX positively regulating expression of an endoplasmic reticulum
XX chaperone gene. bZIP is useful for controlling the expression of
XX endoplasmic reticulum chaperone either positively or negatively in
XX cells and therefore is useful for treatment or prophylaxis of
XX cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
XX wounds and ulcers. bZIP also maintains the correct conformation of
XX the endoplasmic reticulum chaperone and thereby increases the
XX expression of a foreign protein. This sequence taken from the
XX calreticulin (CRT) promoter contains an ERSE like sequence.
XX
XX Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other:
XX
XX Query Match 52.6%; Score 10; DB 21; Length 19;
XX Best Local Similarity 52.6%; Pred. No. 1.4e+03;
XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX QY 1 CCAATNNNNNNNNCCACG 19
XX 1 CCAATGATGTCGACACG 19
XX
XX Db
XX
XX RESULT 19
XX AAA28578
XX ID AAA28578 standard; DNA; 19 BP.
XX
XX AC AAA28578;
XX
XX DT 29-AUG-2000 (first entry)
XX
XX DE Calreticulin promoter ERSE3-like sequence.
XX
XX KM Endoplasmic reticulum stress; ER; transcription factor;
XX transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
XX prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
XX cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;
XX gene expression; GRP; glucose regulated protein; promoter; ss.
XX
XX OS Mus musculus.
XX
XX PN WO200029429-A2.
XX
XX PD 25-MAY-2000.
XX
XX PF 12-NOV-1999; 99WO-JP06305.
XX
XX PR 13-NOV-1998; 98JP-0324227.
XX
XX PR 09-JUN-1999; 99JP-0163112.
XX
XX PA (HSPR-) HSP RES INST INC.
XX
XX PI Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX
XX WPI: 2000-387736/33.
XX
```

XX	New endoplasmic reticulum stress transcription factor (known as bZIP)
PT	for controlling expression of endoplasmic reticulum chaperone, useful
PT	for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT	diseases, wounds and ulcers
XX	
PS	Example 1; Fig 3; 157pp; English.
XX	
CC	An endoplasmic reticulum stress transcription factor (bZIP)
CC	capable of regulating transcription inducing activity exhibited by an
CC	element (ERSE) can be used in a method for controlling expression of
CC	an endoplasmic reticulum chaperone. The method comprises expressing
CC	bZIP. The method can be used for expression of a foreign protein by
CC	positively regulating expression of an endoplasmic reticulum
CC	chaperone gene. bZIP is useful for controlling the expression of
CC	endoplasmic reticulum chaperone either positively or negatively in
CC	cells and therefore is useful for treatment or prophylaxis of
CC	cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
CC	wounds and ulcers. bZIP also maintains the correct conformation of
CC	the endoplasmic reticulum chaperone and thereby increases the
CC	expression of a foreign protein. This sequence taken from the
CC	calreticulin (CRT) promoter contains an ERSE like sequence.
XX	
SO	Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other.
QY	Query Match 52.6%; Score 10; DB 21; Length 19;
	Best Local Similarity 52.6%; Pred. No. 1.4e+03;
	Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
DB	1 CCAATNNNNNNNNCCACG 19
	1 CCAATGAGGCTGACCAACG 19
RESULT 20	
AAA28680	
ID	AAA28680 standard; DNA: 19 BP.
XX	
AC	AAA28680;
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	ERSP1 consensus sequence.
XX	
KW	Endoplasmic reticulum; stress; ER; transcription factor;
KW	transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
KW	prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
KW	cystic fibrosis; ulcer; gene therapy; recombinant gene;
KW	gene expression; GRP; glucose regulated protein; promoter; ss.
XX	
OS	Synthetic.
XX	
PN	WO200029429-A2.
XX	
PD	25-MAY-2000.
XX	
PF	12-NOV-1999; 99WO-JP06305.
XX	
PR	13-NOV-1998; 98JP-0324227.
PR	09-JUN-1999; 99JP-0163112.
XX	
PA	(HSPR-) HSP RES INST INC.
XX	
FI	Haze K, Yoshida H, Mori K, Yanagi H, Yura T;
XX	
DR	WPI; 2000-387736/33.
XX	
PT	New endoplasmic reticulum stress transcription factor (known as bZIP)
PT	for controlling expression of endoplasmic reticulum chaperone, useful
PT	for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
PT	diseases, wounds and ulcers
XX	
PS	Claim 1; Page 130; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein.

Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;

Query Match 52.6%; Score 10; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCAATNNNNNNNNCCACG 19
 1 CCAATNNNNNNNNCCACG 19

RESULT 21
 AAT70001
 ID AAT70001 standard; DNA; 19 BP.
 AC AAT70001;
 XX
 DT 19-DEC-2001 (first entry)
 XX
 DE ERSE consensus sequence.
 XX
 KW ORP150; drug; ischaemic disease; wound; ulcer; diabetes; ERSE;
 KW neurodegenerative disease; cancer; autoimmune disease; promoter; ds.
 XX
 OS Unidentified.
 XX
 PN JP2001238699-A.
 PD 04-SEP-2001.
 XX
 PF 01-MAR-2000; 2000JP-0055384.
 XX
 PR 01-MAR-2000; 2000JP-0055384.
 XX
 PA (HSPk-) HSP KENKYUSHO KK.
 XX
 DR WPI; 2001-610059/70.
 XX
 PT Screening a substance for controlling ORP150 expression, used for
 PT produce drugs for the treatment of diseases associated with ORP150
 PT expression -
 XX
 PS Example 3; Page 9; 9pp; Japanese.
 XX
 CC The present invention relates to a method for screening a substance for
 CC controlling ORP150 expression. The method comprises examining the
 CC expression of a reporter gene product in the presence of a cell strain
 CC transformed by a vector. In the vector, the reporter gene is connected
 CC downstream of the promoter region of ORP150 gene and a sample to be
 CC tested. The method can be used to obtain drug compositions which alter
 CC ORP150 expression. The drug composition can be used for the treatment of
 CC various diseases e.g. ischaemic diseases, wounds, ulcers, diabetes,
 CC neurodegenerative diseases, cancers or autoimmune diseases. The present
 CC sequence is an ERSE consensus sequence which was used in an example from
 CC the present invention.
 XX
 XX Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;

Query Match
Best Local Similarity 52.6%; Score 10; DB 22; Length 19;
Matches 19; Conservative 100.0%; Pred. No. 1.4e+03;
Mismatch 0; Indels 0; Gaps 0;
DB 1 CCAATNNNNNNNNCCACG 19
1 CCAATNNNNNNNNCCACG 19

RESULT 22

AA28780
ID AAF28780 standard; DNA; 19 BP.

AA28780;

09-APR-2001 (first entry)

Endoplasmic response stress element motif.

Cytostatic; antidiabetic; dermatological; hepatotropic; gene therapy;
heterologous gene expression; stress-responsive regulatory sequence;
endoplasmic reticulum stress element; ERSE; glucose responsive protein;
grp78; promoter; cell proliferative disorder; inflammation; cancer;
diabetes; human; transgenic animal; ss.

Unidentified.

Key Location/Qualifiers

protein_bind 1..5
/tag= a
/bound_moiety= "CBF/NF- γ proteins"

misc_feature 6..14
/tag= b
/note= "GC-rich region"

protein_bind 15..19
/tag= c
/bound_moiety= "Y1 protein"

MO200100791-A1.

04-JAN-2001.

28-JUN-2000; 2000MO-US17885.

28-JUN-1999; 99US-0141505.

(UYSC-) UNIV SOUTHERN CALIFORNIA.

Lee AS;

WPI; 2001-071484/08.

A nucleic acid construct comprises a stress-responsive non-coding
regulatory sequence useful in treating and detecting cell proliferative
starvation, e.g. diabetes -

Claim 1; Page 83; 121pp; English.

Targeted gene expression is too used for gene therapy of diseases and
nucleic acid to a host cell; and (2) specific tissue or cell expression
of the heterologous gene. In general, heterologous gene expression has
been controlled in transformed mammalian cells by the constitutive
promoter sequence. Promoters such as these sometimes fail to adequately
express the heterologous gene in a biologically stressed environment.
At least one stress-responsive non-coding regulatory sequence comprising
at least two copies of an endoplasmic reticulum stress element (ERSE).
The preferred ERSE of the invention is the sequence shown here which
corresponds to a glucose responsive protein (grp) 78 gene promoter ERSE.
The construct also comprises a heterologous nucleic acid sequence

operatively linked to the regulatory sequence, where expression of the
heterologous sequence is regulated by the non-coding sequence and where
the heterologous sequence encodes a therapeutic agent effective for
treating a cell proliferative disorder or for treating a disorder
associated with glucose starvation or a detectable marker. The invention
is useful for treating or detecting a cell proliferative disorder
possibly associated with inflammation, for example neoplastic disorders
such as lung cancer, colon-rectum cancer, breast cancer, prostate cancer,
urinary tract cancer, uterine cancer, lymphoma, oral cancer, pancreatic
cancer, leukemia, melanoma, stomach cancer, thyroid cancer, liver cancer,
brain cancer and ovarian cancer. The invention is also useful for
treating a disorder associated with glucose starvation, such as diabetes.
Non-human transgenic animals of the invention include vertebrates such
as rodents, non-human primates, sheep, dogs, cows, pigs, amphibians, and
reptiles.

Sequence 19 BP: 3 A; 5 C; 1 G; 1 T; 9 other;

Query Match
Best Local Similarity 52.6%; Score 10; DB 22; Length 19;
Matches 19; Conservative 100.0%; Pred. No. 1.4e+03;
Mismatch 0; Indels 0; Gaps 0;

DB 1 CCAATNNNNNNNNCCACG 19
1 CCAATNNNNNNNNCCACG 19

RESULT 23

AAA28596
ID AAA28596 standard; DNA; 24 BP.

AAA28596;

29-AUG-2000 (first entry)

GRP78 promoter ERSE1-like sequence.

Endoplasmic reticulum stress; ER; transcription factor;
transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
Kw prophylaxis; cancer; arteriosclerosis; ischemia; wound healing;
Kw cystic fibrosis; ulcer; gene therapy; recombinant gene;
Kw gene expression; GRP; glucose regulated protein; promoter; ss.

Unspecified.

MO200029429-A2.

25-MAY-2000.

12-NOV-1999; 99MO-JP06305.

13-NOV-1998; 98JP-0324227.

09-JUN-1999; 99JP-0163112.

(HSPR-) HSP RES INST INC.

Haze K, Yoshida H, Mori K, Yanagi H, Yura T;

WPI; 2000-387736/33.

New endoplasmic reticulum stress transcription factor (known as bZIP)
for controlling expression of endoplasmic reticulum chaperone, useful
for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
diseases, wounds and ulcers

Example 1; Fig 7; 157pp; English.

An endoplasmic reticulum stress transcription factor (bZIP)
capable of regulating transcription inducing activity exhibited by an
element (ERSE) can be used in a method for controlling expression of
an endoplasmic reticulum chaperone. The method comprises expressing
bZIP. The method can be used for expression of a foreign protein by
positively regulating expression of an endoplasmic reticulum

CC chaperone gene. bzip is useful for controlling the expression of
 CC endoplasmic reticulum chaperone either positively or negatively in
 CC cells and therefore is useful for treatment or prophylaxis of
 CC cancers, arteriosclerosis, cystic fibrosis, ischemic diseases,
 CC wounds and ulcers. bzip also maintains the correct conformation of
 CC the endoplasmic reticulum chaperone and thereby increases the
 CC expression of a foreign protein. This sequence taken from the
 CC glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
 CC sequence.

SO Sequence 24 BP; 5 A; 10 C; 5 G; 4 T; 0 other;

Query Match 52.6%; Score 10; DB 21; Length 24;
 Best Local Similarity 52.6%; Pred. No. 1.5e+03;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 |||||
 DB 5 CCAATCGCGCGCTCCACG 23

RESULT 24
 ABQ00200/c
 ID ABQ00200 standard; DNA: 24 BP.

XX ABQ00200;

DT 11-JUN-2002 (first entry)

DE Oligonucleotide adapter/capture probe 191.

XX Oligonucleotide array; adapter sequence; probe; ss.

OS Synthetic.

XX WO200216649-A2.

PN 28-FEB-2002.

PD 27-AUG-2001; 2001WO-US26519.

PF 25-AUG-2000; 2000US-227948P.

PR 29-AUG-2000; 2000US-228854P.

XX (ILLU-) ILLUMINA INC.

PA Gunderson K;

PI WPI; 2002-292068/33.

DR Array comprising adapter sequences useful for immobilizing or detecting

PT a target nucleic acid sequence, has different addresses comprising

PT different specific capture probes

PS Claim 1; Page 48; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
 CC nucleic acid sequence by attaching a adapter nucleic acid
 CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
 CC nucleic acid and contacting the modified target nucleic acid with (I).
 CC The steps of above method is useful for detecting a target nucleic acid,
 CC which further comprises detecting the presence of the modified target
 CC nucleic acid.

XX Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;

Query Match 52.6%; Score 10; DB 24; Length 24;

Best Local Similarity 52.6%; Pred. No. 1.5e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 |||||

DB 23 CCAATATTACGTGACACG 5

RESULT 25

ABQ04398/c
 ID ABQ04398 standard; DNA: 24 BP.

XX ABQ04398;

DT 11-JUN-2002 (first entry)

DE Oligonucleotide adapter/capture probe 4389.

XX Oligonucleotide array; adapter sequence; probe; ss.

OS Synthetic.

XX WO200216649-A2.

PN 28-FEB-2002.

PD 27-AUG-2001; 2001WO-US26519.

PF 25-AUG-2000; 2000US-227948P.

PR 29-AUG-2000; 2000US-228854P.

XX (ILLU-) ILLUMINA INC.

PA Gunderson K;

PI WPI; 2002-292068/33.

DR Array comprising adapter sequences useful for immobilizing or detecting

PT a target nucleic acid sequence, has different addresses comprising

PT different specific capture probes

PS Claim 1; Page 144; 261pp; English.

XX The invention relates to an oligonucleotide array (I) comprising at least
 CC 25 different addresses (adapter sequences) with each comprising a
 CC different capture probe selected from a group consisting of the sequences
 CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
 CC nucleic acid sequence by attaching a adapter nucleic acid
 CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
 CC nucleic acid and contacting the modified target nucleic acid with (I).
 CC The steps of above method is useful for detecting a target nucleic acid,
 CC which further comprises detecting the presence of the modified target
 CC nucleic acid.

XX Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;

Query Match 52.6%; Score 10; DB 24; Length 24;

Best Local Similarity 52.6%; Pred. No. 1.5e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 |||||

DB 23 CCAATATTACGTGACACG 5

RESULT 26

ABQ04439
 ID ABQ04439 standard; DNA: 24 BP.

XX ABQ04439;

DT 11-JUN-2002 (first entry)

DE Oligonucleotide adapter/capture probe 4430.

XX Oligonucleotide array; adapter sequence; probe; ss.

XX OS Synthetic.
XX PN WO200216649-A2.
XX PD 28-FEB-2002.
XX PF 27-AUG-2001; 2001WO-US26519.
XX PR 25-AUG-2000; 2000US-227948P.
XX PR 29-AUG-2000; 2000US-228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX DR WPI; 2002-292068/33.
XX PT Array comprising adapter sequences useful for immobilizing or detecting
XX PT a target nucleic acid sequence, has different addresses comprising
XX PS different specific capture probes
XX PS Claim 1; Page 144; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid
XX CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX CC nucleic acid and contacting the modified target nucleic acid with (I).
XX CC The steps of above method is useful for detecting a target nucleic acid,
XX CC which further comprises detecting the presence of the modified target
XX CC nucleic acid.
XX SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
XX
XX Query Match
XX Best Local Similarity 52.6%; Score 10; DB 24; Length 24;
XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX Db 1 CCAATNNNNNNNNCCACG 19
XX 11111
XX 2 CCAATATTACGTGACACG 20
XX
XX RESULT 27
XX ABQ10685/C
XX ID ABQ10685 standard; DNA; 24 BP.
XX AC ABQ10685;
XX DT 11-JUN-2002 (first entry)
XX DE Oligonucleotide adapter/capture probe 10676.
XX DE Oligonucleotide adapter/capture probe 10676.
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX OS Synthetic.
XX PN WO200216649-A2.
XX PD 28-FEB-2002.
XX PF 27-AUG-2001; 2001WO-US26519.
XX PR 25-AUG-2000; 2000US-227948P.
XX PR 29-AUG-2000; 2000US-228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX

DR WPI; 2002-292068/33.
XX PT Array comprising adapter sequences useful for immobilizing or detecting
XX PT a target nucleic acid sequence, has different addresses comprising
XX PS different specific capture probes
XX PS Claim 1; Page 221; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid
XX CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX CC nucleic acid and contacting the modified target nucleic acid with (I).
XX CC The steps of above method is useful for detecting a target nucleic acid,
XX CC which further comprises detecting the presence of the modified target
XX CC nucleic acid.
XX SQ Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;
XX
XX Query Match
XX Best Local Similarity 52.6%; Score 10; DB 24; Length 24;
XX Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX
XX Db 1 CCAATNNNNNNNNCCACG 19
XX 11111
XX 23 CCAATATTACGTGACACG 5
XX
XX RESULT 28
XX ABQ10726
XX ID ABQ10726 standard; DNA; 24 BP.
XX AC ABQ10726;
XX DT 11-JUN-2002 (first entry)
XX DE Oligonucleotide adapter/capture probe 10717.
XX DE Oligonucleotide adapter/capture probe 10717.
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX OS Synthetic.
XX PN WO200216649-A2.
XX PD 28-FEB-2002.
XX PF 27-AUG-2001; 2001WO-US26519.
XX PR 25-AUG-2000; 2000US-227948P.
XX PR 29-AUG-2000; 2000US-228854P.
XX PA (ILLU-) ILLUMINA INC.
XX PI Gunderson K;
XX DR WPI; 2002-292068/33.
XX PT Array comprising adapter sequences useful for immobilizing or detecting
XX PT a target nucleic acid sequence, has different addresses comprising
XX PS different specific capture probes
XX PS Claim 1; Page 221; 261pp; English.
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX CC 25 different addresses (adapter sequences) with each comprising a
XX CC different capture probe selected from a group consisting of the sequences
XX CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
XX CC nucleic acid sequence by attaching a adapter nucleic acid
XX CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX CC nucleic acid and contacting the modified target nucleic acid with (I).
XX CC The steps of above method is useful for detecting a target nucleic acid,

CC which further comprises detecting the presence of the modified target
 CC nucleic acid.

XX Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
 SQ

Query Match 52.6%; Score 10; DB 24; Length 24;
 Best Local Similarity 52.6%; Pred. No. 1.5e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
 |||||
 DB 2 CCAATATTACGTGACCAGC 20

RESULT 29
 AAV45529/c
 ID AAV45529 standard; DNA; 25 BP.

AAV45529;

15-FEB-1999 (first entry)

Helicobacter pylori ureg gene PCR primer.

Vaccine; antigen; antigen; toxin; diagnosis; gastritis; ulcer;

stomach cancer; ureg gene; PCR; primer; ss.

Synthetic.

Helicobacter pylori.

WO9844130-A1.

08-OCT-1998.

31-MAR-1998; 98WO-KR00073.

31-MAR-1997; 97KR-0011951.

31-MAR-1997; 97KR-0011950.

(DAEW-) DAEWONG PHARM CO LTD.

Choi D, Jung H, Kim B, Park M, Shin S, Yu Y;

WPI; 1998-568279/48.

New chimeric proteins for use against Helicobacter pylori

comprising an antigenic protein of H. pylori and A1 and B subunits

of Vibrio cholerae toxin, preferably produced by recombinant

techniques

Example 2-15; Page 13; 102pp; English.

PCR primers (see AAV45529 and AAV45530) are designed for the PCR

amplification of the Helicobacter pylori ureg gene. The invention

relates to recombinant DNA (see AAV62460-61) comprising a fusion gene

prepared by ligating an antigenic determinant coding gene (e.g. the

ureg gene) of H. pylori and A2 and B subunit genes of Vibrio

cholerae. Also claimed are chimeric proteins (see AAW60599-600)

encoded by such recombinant DNAs, methods for the recombinant

production of the chimeric proteins, and use of the chimeric

proteins in preventative and therapeutic vaccines for H. pylori-

associated diseases such as gastritis, gastric ulcer, duodenal

ulcer and gastric cancer.

Sequence 25 BP; 7 A; 2 C; 8 G; 8 T; 0 other;

Query Match 52.6%; Score 10; DB 19; Length 25;
 Best Local Similarity 52.6%; Pred. No. 1.5e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 30
 AB012221/c
 ID AB012221 standard; DNA; 25 BP.

AB012221;

11-JUN-2002 (first entry)

Oligonucleotide adapter/capture probe 12212.

Oligonucleotide array; adapter sequence; probe; ss.

Synthetic.

WO200216649-A2.

28-FEB-2002.

27-AUG-2001; 2001WO-US26519.

25-AUG-2000; 2000US-227948P.

29-AUG-2000; 2000US-228854P.

(ILLU-) ILLUMINA INC.

Gundersen K;

WPI; 2002-292068/33.

Array comprising adapter sequences useful for immobilizing or detecting

a target nucleic acid sequence, has different addresses comprising

different specific capture probes

Claim 1; Page 240; 261pp; English.

The invention relates to an oligonucleotide array (I) comprising at least

25 different addresses (adapter sequences) with each comprising a

different capture probe selected from a group consisting of the sequences

given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target

nucleic acid sequence by attaching a adapter nucleic acid

(ABQ00010-ABQ13409) to a target nucleic acid to form a modified target

nucleic acid and contacting the modified target nucleic acid with (I).

The steps of above method is useful for detecting a target nucleic acid,

which further comprises detecting the presence of the modified target

nucleic acid.

Sequence 25 BP; 4 A; 5 C; 9 G; 7 T; 0 other;

Query Match 52.6%; Score 10; DB 24; Length 25;
 Best Local Similarity 52.6%; Pred. No. 1.5e+03;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
 |||||
 DB 24 CCAATATTACGTGACCAGC 6

Search completed: November 16, 2002, 02:15:58

Job time : 260 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 02:09:22 ; Search time 1972 Seconds
(without alignments)
156.042 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19
Sequence: 1 ccaatnnnnnnnnccacg 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 90 summaries

Database :

EST:*
1: em_estba:*
2: em_estbm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estp1:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	52.6	43	17	BH857113
2	10	52.6	76	9	AA475936
3	10	52.6	79	14	B0756881
4	10	52.6	80	17	BH251489
5	10	52.6	82	14	B0099298
6	10	52.6	86	17	BH232183

C 7	10	52.6	97	17	BH222106	BH222106 1006105C1
C 8	10	52.6	99	17	AZ921866	AZ921866 HRCot4D10
C 9	10	52.6	100	12	BF086094	BF086094 CM3-GN005
C 10	10	52.6	101	17	BH583741	BH583741 BOGXN16TR
C 11	10	52.6	103	9	AA927925	AA927925 OM23B01.5
C 12	10	52.6	109	17	BH864991	BH864991 SALK_0972
C 13	10	52.6	110	12	BF094257	BF094257 CM4-UT004
C 14	10	52.6	110	17	AZ720239	AZ720239 RPCI-24-1
C 15	10	52.6	113	17	BH222899	BH222899 1006109HO
C 16	10	52.6	115	9	A1938545	A1938545 SB55D02.Y
C 17	10	52.6	115	10	AW945325	AW945325 PM3-EN000
C 18	10	52.6	115	13	BG950375	BG950375 CM3-CT060
C 19	10	52.6	115	17	AG024826	AG024826 Oryza sat
C 20	10	52.6	119	9	A1549504	A1549504 UI-R-C3-E
C 21	10	52.6	120	17	BH230343	BH230343 1006157D1
C 22	10	52.6	121	17	BH222096	BH222096 1006105C0
C 23	10	52.6	123	9	AA405167	AA405167 zUS101.r
C 24	10	52.6	124	17	AQ073902	AQ073902 EP(3)3309
C 25	10	52.6	124	17	BH812753	BH812753 SALK_0630
C 26	10	52.6	124	17	BH847929	BH847929 SALK_0660
C 27	10	52.6	129	17	AZ919927	AZ919927 1006017C0
C 28	10	52.6	130	17	BH895687	BH895687 3526.1.35
C 29	10	52.6	132	12	BE936064	BE936064 QV2-NN005
C 30	10	52.6	132	12	BF361951	BF361951 QV2-NN004
C 31	10	52.6	132	17	BH753521	BH753521 SALK_0292
C 32	10	52.6	132	17	BH854781	BH854781 SALK_0886
C 33	10	52.6	133	17	AZ726948	AZ726948 RPCI-24-1
C 34	10	52.6	135	10	AV963893	AV963893 AV963893
C 35	10	52.6	137	9	AA168302	AA168302 ms54a10.r
C 36	10	52.6	137	13	BM645289	BM645289 170006873
C 37	10	52.6	138	10	BE002165	BE002165 PM2-BN008
C 38	10	52.6	140	9	AV060848	AV060848 AV060848
C 39	10	52.6	141	10	AV957023	AV957023 AV957023
C 40	10	52.6	143	10	AV368329	AV368329 AV368329
C 41	10	52.6	145	9	A1843919	A1843919 UI-M-AP1
C 42	10	52.6	145	10	BE151291	BE151291 CM1-HT028
C 43	10	52.6	146	10	AM449763	AM449763 UI-H-B13
C 44	10	52.6	146	12	BG431131	BG431131 602498760
C 45	10	52.6	148	10	AM121751	AM121751 UI-M-BH2
C 46	10	52.6	148	10	BE115188	BE115188 UI-R-B11
C 47	10	52.6	149	10	BB606552	BB606552 BB606552
C 48	10	52.6	149	17	BH229683	BH229683 100615360
C 49	10	52.6	150	17	AZ973950	AZ973950 2M0248823
C 50	10	52.6	152	17	BH197483	BH197483 TC3-59E3
C 51	10	52.6	152	17	BH790242	BH790242 SALK_0566
C 52	10	52.6	155	9	AV010555	AV010555 AV010555
C 53	10	52.6	155	10	AW371361	AW371361 RC0-BT028
C 54	10	52.6	156	10	AM091112	AM091112 614090E11
C 55	10	52.6	156	10	BB786641	BB786641 BB786641
C 56	10	52.6	157	9	A1817561	A1817561 WK24Q07.X
C 57	10	52.6	158	9	A1964826	A1964826 ZP-EP327
C 58	10	52.6	158	12	BE712044	BE712044 QV2-HT069
C 59	10	52.6	159	9	AJ237134	AJ237134 AJ237134
C 60	10	52.6	159	9	AV289314	AV289314 AV289314
C 61	10	52.6	159	13	BI399749	BI399749 MI-P-AV1
C 62	10	52.6	159	13	BI406859	BI406859 182D02.Ma
C 63	10	52.6	161	13	BI059548	BI059548 IL3-PT011
C 64	10	52.6	163	13	BI742019	BI742019 Kt84G06.Y
C 65	10	52.6	164	13	BI023913	BI023913 MR3-MT032
C 66	10	52.6	165	12	BG090373	BG090373 mac19h08
C 67	10	52.6	167	10	BF749006	BF749006 MR2-BN038
C 68	10	52.6	167	10	BB001165	BB001165 BB001165
C 69	10	52.6	168	9	AA749830	AA749830 ISAS0335
C 70	10	52.6	168	9	A1846641	A1846641 UI-M-NT1
C 71	10	52.6	168	10	BE087363	BE087363 QV1-BT068
C 72	10	52.6	169	13	BI088613	BI088613 602853166
C 73	10	52.6	170	12	BF733308	BF733308 MR0-AN003
C 74	10	52.6	170	13	BI799942	BI799942 H144C07.E
C 75	10	52.6	171	13	BI047605	BI047605 MR4-ST024
C 76	10	52.6	171	9	AV060234	AV060234 AV060234
C 77	10	52.6	172	9	AV086215	AV086215 AV086215
C 78	10	52.6	172	13	BM195701	BM195701 C0315A05
C 79	10	52.6	173	9	AA684809	AA684809 EST105472

C	80	10	52.6	173	12	BF748094	MR2-BN038
	81	10	52.6	173	17	BH789270	SALK_0014
C	82	10	52.6	174	9	AV004354	AV004354
	83	10	52.6	174	13	BJ121753	BJ121753
C	84	10	52.6	174	17	BH89513	3526_1_34
	85	10	52.6	175	9	AV022317	AV022317
	86	10	52.6	175	9	AA562236	AA562236
	87	10	52.6	175	17	BH855839	vo30110.1
	88	10	52.6	176	12	BF347768	SALK_0844
C	89	10	52.6	178	9	AI937584	BF347768 602020656
	90	10	52.6	178	9	AV097435	AI937584 WP81C04.X
							AV097435 AV097435

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION
BH857113	BH857113	43 bp DNA linear GSS 08-JUL-2002
	SAIK_076621.44.95.x	Arabidopsis thaliana TRNA insertion lines

ACCESSION	BH857113
VERSION	BH857113.1
KEYWORDS	GSS.
SOURCE	thale cress.

ORGANISM

REFERENCE
AUTHORS
1 (bases 1 to 43)
Alonso, J.M., leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab

TITLE	A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL	Arabidopsis Genome
COMMENT	Unpublished (2001)
	Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel.: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckere@salk.edu
This is single pass sequence recovered from the left border of
tDNA. This sequence lies within an annotated exon of At4g29100.
Class: tDNA tagged.

FEATURES	Location/Qualifiers
source	1. .43

```

/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/olone="SAUK_076821.44.95.x"
/olone_1ib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

```

Query Match	52.68;	Score 10;	DB 17;	Length 43;
Best Local Similarity	52.68;	Pred. No.	1.5e+04;	

QY	1	CCAATNNNNNNNNCCACG	19
Db	18	CCAATGAATTACGCCACG	36

RESULT 2

AA475936					
LOCUS	AA475936	76 bp	mRNA	linear	EST 18-JUN-1997
DEFINITION	th25b10.r1 Soares_mammary-gland.NbMxg Mus musculus cDNA clone				

IMAGE:8/64/5 5' similar to TR:EI96/49 EI96/49 mRNA; EXPRESSED
SEQUENCE TAG ; mRNA sequence.
147000

ACCESSION	AA475936	
VERSION	AA475936.1	GI:2203787
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 76)
Merrit, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouque, T.

TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project

WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.

FEATURES	Location/Qualifiers
source	1. .76

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="876475"
/clone_lib="Soares_mammary_gland_NBMC"
/tissue="male"
/tissue_type="mammary_gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Organ: mammary gland; Vector: pUT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)

```

BASE COUNT

a	19	c	28	g	16	t	13
---	----	---	----	---	----	---	----

```

Query Match:      52.6%;      Score 10; DB 9; Length 76;
Best Local Similarity 52.6%;      Pred. No. 1.9e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATTNNNNNNNNCCACG 19
    |||||
Db 40 CCAATGCTTTAGCGCCACG 58

```

RESULT 3			
B0756881			
LOCUS			
DEFINITION			
B0756881	79 bp	mRNA	linear
EBem09_SQ005_E15_R	embryo, 1 Day	germination, no treatment, cv	EST 26-JUL-2002

optic, EBem09 Hordeum vulgare cDNA clone EBem09_SQ005_E15 5', mRNA

Sequence.
 accession BO756881 GI:21965353
 version BO756881.1
 keywords EST.
 source Hordeum vulgare.
 organism Hordeum vulgare.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae

REFERENCE
 AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
 TITLE Development of Barley Transcriptome Resources
 JOURNAL Unpublished (2001)
 COMMENT Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: estescr@sari.ac.uk.

FEATURES
 source
 1..79
 /organism="Hordeum vulgare"
 /cultivar="Optic"
 /db_xref="taxon:4513"
 /clone="EBem09_SQ005_E15"
 /clone_lib="Embryo, 1 Day germination, no treatment, cv
 Optic, EBem09"
 /issue_type="embryo"
 /dev_stage="1 Day germination"
 /lab_host="DH10B"
 /note="Vector: pSPORT1. Site_1: Sal I; Site_2: Not I;
 Non-normalised library; directionally cloned into pSPORT1.
 Derived from embryos dissected from germinating grains (1
 day) in glasshouse grown barley plants. Developed as part
 of the barley transcriptome resources of BBSRC/SERAD
 funded cereal ICG (Investigating Gene Function) project."

BASE COUNT
 19 a 18 c 17 g 25 t

ORIGIN

Query Match 52.6%; Score 10; DB 14; Length 79;
 Best Local Similarity 52.6%; Pred. No. 1.9e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 42 CCAATTTGTCAACACG 60

RESULT 4
 LOCUS BH251489 80 bp DNA linear GSS 28-NOV-2001
 DEFINITION SALK_011672 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_011672, DNA sequence.
 accession BH251489
 version BH251489.1 GI:17138467
 keywords GSS.
 source thale cress.
 organism Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 80)
 Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriab,
 C., Jeske, A., Kaines, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
 Zimmerman, J., and Ecker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies

TITLE
 JOURNAL
 COMMENT

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: eckersalk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..80
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_011672"
 /clone_lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT
 18 a 20 c 21 g 19 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 80;
 Best Local Similarity 52.6%; Pred. No. 1.9e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 26 CCAATGATTAATAGCCACG 8

RESULT 5
 LOCUS BQ099298 82 bp mRNA linear EST 10-APR-2002
 DEFINITION pn28h02.y2 Ostertagia ostertagi L3 PAMPI v1 Ostertagia ostertagi
 cDNA 5', mRNA sequence.
 accession BQ099298
 version BQ099298.1 GI:20132282
 keywords EST.
 source Ostertagia ostertagi.
 organism Ostertagia ostertagi.
 Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongylida;
 Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia.

REFERENCE
 AUTHORS McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J., Wylie, T.,
 Dante, M., Maira, M., Hillier, L., Kucaba, T., Pfeising, B., Bowers, Y.,
 Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarelis, V.,
 Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe,
 M., Allen, M., Person, B., Swaller, T., Harvey, N., Schuck, R., Kohn, S.,
 Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
 Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter, JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estelw@wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. DNA Sequencing by: Washington
 University Genome Sequencing Center
 High quality sequence stop: 69.
 Location/Qualifiers
 1..82
 /organism="Ostertagia ostertagi"
 /db_xref="taxon:6317"
 /clone_lib="Ostertagia ostertagi L3 PAMPI v1"
 /dev_stage="L3"
 /lab_host="DH10B"
 /note="Vector: PAMPI (Gibco); Site_1: NotI; Site_2: SalI;

The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Louis Gasbarre of the USDA, Beltsville, MD (lgsbarre@nrl.barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of *Osteria* eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen."

BASE COUNT 24 a 24 c 12 g 22 t
ORIGIN

Query Match 52.6%; Score 10; DB 14; Length 82;
Best Local Similarity 52.6%; Pred. No. 1.9e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 12 CCAATGAGAGTGTCCAGC 30

RESULT 6
BH232183/c 86 bp DNA linear GSS 08-NOV-2001
LOCUS 1006166D12.y1 1006 - Rescemu Grid G Zea mays genomic, DNA
DEFINITION
sequence.

ACCESSION BH232183
VERSION BH232183.1 GI:16837119
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
1 (bases 1 to 86)
Walbot,V.

AUTHORS Maize genomic sequences found using engineered Rescemu transposon
TITLE Unpublished (2001)
JOURNAL Contact: Walbot V
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006166 row: 23
Class: transposon-tagged.

FEATURES

source

Location/Qualifiers
1..86
/organism="Zea mays"
/cultiivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - Rescemu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescemu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII;
Rescemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescemu.' Grid G was grown at Stanford in 2000. DNA was

extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 13 a 24 c 37 g 12 t
ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 86;
Best Local Similarity 52.6%; Pred. No. 2e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 61 CCAATCATTTGAGCCAGC 43

RESULT 7
BH222106/c 97 bp DNA linear GSS 08-NOV-2001
LOCUS 1006105C10.x1 1006 - Rescemu Grid G Zea mays genomic, DNA
DEFINITION
sequence.

ACCESSION BH222106
VERSION BH222106.1 GI:16816606
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
1 (bases 1 to 97)
Walbot,V.

AUTHORS Maize genomic sequences found using engineered Rescemu transposon
TITLE Unpublished (2001)
JOURNAL Contact: Walbot V
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site found so sequence was trimmed.
Post-ligation sequence submitted separately.
Plate: 1006105 row: 13
Class: transposon-tagged.

FEATURES
source
Location/Qualifiers
1..97
/organism="Zea mays"
/cultiivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - Rescemu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: Rescemu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII;
Rescemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 11 a 27 c 44 g 15 t
ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 97;
Best Local Similarity 52.6%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAGC 19

Db 92 CCAATTCGAGCACCACG 74

RESULT 8 A2921866/c 99 bp DNA linear GSS 07-JUN-2002

LOCUS A2921866 Sorghum bicolor HRCot Sorghum bicolor genomic DNA

DEFINITION sequence

ACCESSION A2921866

VERSION A2921866.1 GI:13400225

KEYWORDS GSS.

SOURCE sorghum.

ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

Clade: Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 99)

Peterson, D.G., Schulze, S.R., Sclata, E.B., Lee, S.A., Bowers, J.E.,

Nagel, A., Jiang, N., Tibbitts, D.C., Messler, S.R., and Peterson, A.H.

Integration of Cot analysis, DNA cloning, and high-throughput

sequencing facilitates genome characterization and gene discovery

Genome Res. 12 (5), 795-807 (2002)

JOURNAL 21992826

COMMENT Contact: Peterson DG

Plant Genome Mapping Laboratory

University of Georgia

Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA

30602, USA

Tel: 706-583-0167

Fax: 706-583-0160

Email: dgp@arches.uga.edu

Class: Hydroxyapatite-fractionated DNA.

Location/Qualifiers

1..99

/organism="Sorghum bicolor"

/cultivar="BTx623"

/db_xref="taxon:4558"

/clone_lib="Sorghum bicolor HRCot"

/issue_type="leaves"

/dev_stage="seedling"

/note="Vector: pGEM-TA-Easy; A Cot analysis was performed

for the sorghum genome. Based on the resulting Cot curve,

hydroxyapatite chromatography was used to isolate

'highly-repetitive' (HR), 'moderately-repetitive' (MR),

and 'single/low-copy' (SL) sequence components from

sheared genomic DNA. The three repetition-based DNA

components were cloned into E. coli to produce HRCot,

MRCot, and SLCot genomic libraries. Blotting and

sequencing data indicates that each library is

representative of the component from which it was derived.

Putative ID listings given for sequences are based on

comparison (blastn) with sequences in the NCBI Nr

database. Only the primary match is given (all primary E

values are < or = 1.00E-5). In no instance does a 'Cot

clone' contain the complete sequence of its putative Nr

match."

BASE COUNT 18 a 19 c 29 g 33 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 99;

Best Local Similarity 52.6%; Pred. No. 2.1e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAGC 19

Db 56 CCAATTCGATCTCCACG 38

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ACCESSION BF086094

VERSION BF086094.1 GI:10891804

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 100)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Nagel, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2=CM3-GN0052-080

900-334-cl1&ts=2000-09-08&tl=1)

Seq primer: puc 18 forward

High quality sequence start: 5

High quality sequence stop: 100.

Location/Qualifiers

1..100

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="GN0052"

/dev_stage="adult"

/note="Organ: placenta normal; Vector: puc18; Site: 1; SmaI

: Site: 2; SmaI; A mini-library was made by cloning

products derived from ORSPMS PCR (U.S. Letters Patent

application No. 196,776 - Ludwig Institute for Cancer

Research) profiles into the pUC 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT 35 a 23 c 18 g 24 t

ORIGIN

Query Match 52.6%; Score 10; DB 12; Length 100;

Best Local Similarity 52.6%; Pred. No. 2.1e+04;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAGC 19

Db 82 CCAATTCGATCCACG 100

|||||

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|||||

|||||

|||||

|||||

|||||

|||||

RESULT 10 BH583741 101 bp DNA linear GSS 15-DEC-2001

LOCUS BH583741 BGCX Brassica oleracea genomic clone BGCXN16, DNA

DEFINITION sequence.

ACCESSION BH583741

VERSION BH583741.1 GI:17836198

KEYWORDS GSS.

SOURCE Brassica oleracea.

ORGANISM Brassica oleracea.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 101)

Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.

REFERENCE

AUTHORS

TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source location/Qualifiers

1..101
/organism="Brassica oleracea"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone.lib="BOGXN16"
/note="Vector: PHOS1, site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"
BASE COUNT 38 a 23 c 22 g 18 t
ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 101;
Best Local Similarity 52.6%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 25 CCAATGCGGCGCCACG 43

RESULT 11
AA927925/c 103 bp mRNA linear EST 10-JUN-1998
LOCUS om23b01.s1 Soares_NFL.T.GBC.S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1541833 3', mRNA sequence.
ACCESSION AA927925
VERSION AA927925.1 GI:3076669
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 103)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
Tumor Gene Index
Unpublished (1997)
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seg. primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 57.

FEATURES
source location/Qualifiers

1..103
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone.lib="IMAGE:1541833"
/lab_host="DH10B"
/note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19w, testis NHT, and B-cell NCI CGAP CCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239.

BASE COUNT 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo.
ORIGIN 25 a 23 c 25 g 30 t

Query Match 52.6%; Score 10; DB 9; Length 103;
Best Local Similarity 52.6%; Pred. No. 2.1e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 55 CCAATTCATCGACACG 37

RESULT 12
BH864991/c 109 bp DNA linear GSS 05-AUG-2002
LOCUS SALK_097225 Arabidopsis thaliana TDNA insertion lines Arabidopsis
DEFINITION BH864991 thaliana genomic clone SALK_097225, DNA sequence.
ACCESSION BH864991
VERSION BH864991.1 GI:22100889
KEYWORDS GSS.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 109)
Alonso, J.M., Leisste, F.J., Barajas, P., Chen, H., Cheuk, R., Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
JOURNAL Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
CLASS: TDNA tagged.

FEATURES
source location/Qualifiers

1..109
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone.lib="SALK_097225"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
BASE COUNT 22 a 29 c 24 g 34 t
ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 109;
Best Local Similarity 52.6%; Pred. No. 2.2e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 30 CCAATGTAAGACGACG 12

RESULT 13
BF094257 110 bp mRNA linear EST 19-OCT-2000
LOCUS BF094257
DEFINITION CM4-UT0042-050900-568-e11 UT0042 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF094257
 VERSION BF094257.1 GI:10899967
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 110)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE Shocgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=4t2-CM4-UT0042-050>)
 Seq primer: puc 18 forward
 High quality sequence start: 12
 High quality sequence stop: 109.
 Location/Qualifiers
 1..110
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="UT0042"
 /dev_stage="Adult"
 /note="Organ: uterus; tumor; Vector: puc18; Site: 1; SmaI; Site: 2; SmaI: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
 ORIGIN 26 a 38 c 23 g 23 t

Query Match 52.6%; Score 10; DB 12; Length 110;
 Best Local Similarity 52.6%; Pred. No. 2.2e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 5 CCAATCCCTTACTCCACG 23

RESULT 14
 A2720239 110 bp DNA linear GSS 24-JAN-2001
 LOCUS A2720239
 DEFINITION RPCI-24-104K1.TV RPCI-24 Mus musculus genomic clone RPCI-24-104K1,
 DNA sequence.
 A2720239
 ACCESSION A2720239.1 GI:12461733
 VERSION
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 110)
 Zhao, S., Niernan, W., Malek, J., Shatsman, S., Akimov, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,

TITLE Russell, D., de Jong, P. and Fraser, C.M.
 JOURNAL Mouse BAC End Sequences from Library RPCI-24
 COMMENT Unpublished (1999)
 Other GSSs: RPCI-24-104K1.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tldb/bac-ends/mouse/bac_end_intro.html
 Plate: 104 row: K column: 1
 Seq primer: T7
 Class: BAC ends.
 Location/Qualifiers
 1..110
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-104K1"
 /clone_lib="RPCI-24"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /note="Vector: pTRABAC1; Site: 1: BamHI; Site: 2: BamHI; RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pTRABAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

BASE COUNT
 ORIGIN 28 a 28 c 15 g 39 t

Query Match 52.6%; Score 10; DB 17; Length 110;
 Best Local Similarity 52.6%; Pred. No. 2.2e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 52 CCAATCTTTTCATCCACG 70

RESULT 15
 BH222899/c 113 bp DNA linear GSS 08-NOV-2001
 LOCUS BH222899
 DEFINITION 1006109H01.x1 1006 - Rescuemu Grid G Zea mays genomic, DNA
 sequence.
 BH222899
 ACCESSION BH222899.1 GI:16818250
 VERSION
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays

REFERENCE
 AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 JOURNAL clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 113)
 Walbot, V.
 Maize genomic sequences found using engineered Rescuemu transposon
 UNPUBLISHED (2001)
 CONTACT: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site so sequence was trimmed. Post-ligation
 sequence submitted separately.
 Plate: 1006109 row: 15
 Class: transposon-tagged.

FEATURES

Source

Location/Qualifiers

1. .113

/organism="Zea mays"

/cultivar="mixed background W23/Al88/B73"

/db_xref="taxon:4577"

/clone_lib="1006 - RescueMu Grid G"

/tissue_type="leaf"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT

8 a 19 c 50 g 36 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 113;
Best Local Similarity 52.6%; Pred. No. 2.2e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 23 CCAATCCACGACGACG 5

RESULT 16

AI938545

LOCUS

AI938545 115 bp mRNA linear EST 30-NOV-2001

DEFINITION

sb55b02.y1 Gm-cl018 Glycine max cDNA clone GENEOME SYSTEMS CLONE ID: Gm-cl018-4 5' similar to TR:Q38910 Q38910 XYLOGLUCAN

ACCESSION

AI938545

VERSION

AI938545.1 GI:5677415

KEYWORDS

EST.

SOURCE

soybean.

ORGANISM

Glycine max

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaceae; Glycine.

REFERENCE

1 (bases 1 to 115)

AUTHORS

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Maria, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE

Public Soybean EST Project

JOURNAL

Unpublished (1999)

COMMENT

Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Possible reversed clone: similarity on wrong strand This clone is available through: Resgen, Invitrogen Corp, 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-353-4363 or contact via email: ccuteresgen.com
Insert Length: 661 Std Error: 0.00
High quality sequence stop: 1.
Location/Qualifiers
1. .115
/organism="Glycine max"

FEATURES

Source

/organism="Glycine max"

/db_xref="taxon:3847"
/clone_lib="Gm-cl018-4"

/tissue_type="leaves of greenhouse grown plants"

/dev_stage="2-3 weeks old"

/lab_host="DH10B (Gibco BRL)"

/note="Vector: pBluescript II Xr; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II Xr library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT

33 a 33 c 25 g 24 t

ORIGIN

Query Match 52.6%; Score 10; DB 9; Length 115;
Best Local Similarity 52.6%; Pred. No. 2.2e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 1 CCAATCAGTGGACGACG 19

RESULT 17

AM945325

LOCUS

AM945325 115 bp mRNA linear EST 31-MAY-2000

DEFINITION

PM3-EN0004-280400-001-g04 EN0004 Homo sapiens cDNA, mRNA sequence.

ACCESSION

AM945325

VERSION

AM945325.1 GI:8123078

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 115)

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Bioness, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3-EN0004-280400-001-g04&ts=2000-04-28&td=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 114.
Location/Qualifiers
1. .115
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone.lib="EN0004"		/dev.stige="Adult"	
/note="Organ: lung-normal; Vector: puc18; Site.1: SmaI; Site.2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
BASE COUNT	37 a 21 c 25 g 32 t		
ORIGIN			
Query Match	52.6%;	Score 10;	DB 10; Length 115;
Best Local Similarity	52.6%;	Pred. No. 2.2e+04;	
Matches	10; Conservative	0; Mismatches	9; Indels 0; Gaps 0;
QY	1 CCAATNNNNNNNNCCAGC 19		
DB	23 CCAATTCAATAGTCACG 5		
RESULT 19			
LOCUS	AG024826	115 bp	DNA linear
DEFINITION	Oryza sativa (japonica cultivar-group) DNA, clone: T02869T, genomic flanking sequence of Tos17 insertion in rice strain NC0370, genomic survey sequence.		
ACCESSION	AG024826		
VERSION	AG024826.1	GI:7683490	
KEYWORDS	GSS.		
SOURCE	Oryza sativa (japonica cultivar-group) (strain: NC0370, cultivar: Nipponbare) DNA, clone.lib: PCR product directly amplified from rice genomic DNA clone: T02869T.		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	1 Miyao, A., and Hirochika, H. Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: Ehrhartoideae; Oryzaceae; Oryza.		
AUTHORS	1 Miyao, A. and Hirochika, H.		
TITLE	Rice insertion mutants		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 115)		
AUTHORS	Miyao, A., Miyazaki, A., Yamashita, Y. and Hirochika, H.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-OCT-1999) Akio Miyao, National Institute of Agrobiological Sciences, Molecular Genetics, 2-1-2, Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: miyao@affrc.go.jp, URL: http://tos.nias.affrc.go.jp/, Tel: 81-298-38-7020, Fax: 81-298-38-7020)		
FEATURES			
source	1..115		
location/Qualifiers	/organism="Oryza sativa (japonica cultivar-group)"		
BASE COUNT	44 a 26 c 17 g 23 t	5 others	
ORIGIN			
Query Match	52.6%;	Score 10;	DB 17; Length 115;
Best Local Similarity	52.6%;	Pred. No. 2.2e+04;	
Matches	10; Conservative	0; Mismatches	9; Indels 0; Gaps 0;
QY	1 CCAATNNNNNNNNCCAGC 19		
DB	85 CCAATTAAAGTAACACG 103		
RESULT 20			
LOCUS	A1549504/C	119 bp	mRNA linear
DEFINITION	UI-R-C3-tu-f-02-0-UI-s1 UI-R-C3 Rattus norvegicus cDNA clone		
ACCESSION	A1549504		
VERSION	A1549504.1	GI:4466992	
KEYWORDS	EST.		
SOURCE	Norway rat.		
ORGANISM	Rattus norvegicus		
REFERENCE	1 Rattus norvegicus		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		

REFERENCE 1 (bases 1 to 119)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.waeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA library preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
 Seq primer: M13 forward.
 FEATURES
 SOURCE Location/Qualifiers
 1..119
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-C3-tu-f-02-0-UI"
 /clone_1lb="UI-R-C3"
 /dev_stage="adult"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-C3 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, muscle, and 8, 12 and 18-day embryos, after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-C3) was constructed as follows: pCpamplified cDNA inserts from UI-R-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)."

BASE COUNT 23 a 20 c 32 g 44 t
 ORIGIN

Query Match 52.6%; Score 10; DB 9; Length 119;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCAGC 19
 |||||
 Db 119 CCAATGCTTACTCCACG 101

RESULT 21 120 bp DNA linear GSS 08-NOV-2001
 BH230343
 LOCUS 1006157D12.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
 DEFINITION
 ACCESION BH230343
 VERSION BH230343.1 GI:16833394

KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 120)
 AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Very probable ligation site found so sequence was trimmed.
 Post-ligation sequence submitted separately.
 Plate: 1006157 row: 13
 Class: transposon-tagged.
 FEATURES
 SOURCE Location/Qualifiers
 1..120
 /organism="Zea mays"
 /cultivar="mixed background W23/A18/B73"
 /db_xref="taxon:4577"
 /clone_1lb="1006 - RescueMu Grid G"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: Leaf; Vector: RescueMu (engineered from Bluescript backbone); Site 1: BamHI; Site 2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 12 a 31 c 51 g 26 t
 ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 120;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CCAATNNNNNNNNCCAGC 19
 |||||
 Db 91 CCAATTCAAGCACCACG 73

RESULT 22 121 bp DNA linear GSS 08-NOV-2001
 BH222096
 LOCUS 1006105C05.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
 DEFINITION
 ACCESION BH222096
 VERSION BH222096.1 GI:16816585
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 121)
 AUTHORS Walbot,V.
 TITLE Maize genomic sequences found using engineered RescueMu transposon
 JOURNAL unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences

Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006105 row: 13
Class: transposon-tagged.

FEATURES

SOURCE

1. 121
/organism="Zea mays"
/cultivar="mixed background W23/A18/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site.1: BamHI; Site.2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu', 'Grid G' was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin." 51 g 25 t

BASE COUNT

12 a 33 c 51 g 25 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 121;
Best Local Similarity 52.6%; Pred. No. 2.3e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 92 CCAATTCGACGCCACCAGC 74

RESULT 23 123 bp mRNA linear EST 17-MAY-1997
AA405167
LOCUS z51101.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:741553 5', mRNA sequence.

ACCESSION AA405167
VERSION AA405167.1 GI:2063527
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 (bases 1 to 123)
Hillier L., Allen M., Bowles L., Dubuque T., Geisler G., Jost S.,
Kucaba T., Lacy M., Le N., Lennon G., Marra M., Martin J., Moore B.,
Schellenberg R., Stepien M., Tan F., Theising B., White Y., Wyllie
, T., Waterston R. and Wilson R.
WashU-Merck EST Project 1997

TITLE

JOURNAL

COMMENT

Unpublished (1997)
Contact: Wilson R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: estewartson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham.

FEATURES

SOURCE

1. 123
/organism="Homo sapiens"

/db_xref="GDB:5941690"
/db_xref="taxon:9606"
/clone_lib="IMAGE:741553"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer (5'
TGTACCAATCTGAGAGTGGAGCGCGCGGCTTTTCTTTTCTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo."

BASE COUNT

23 a 37 c 27 g 36 t

ORIGIN

Query Match 52.6%; Score 10; DB 9; Length 123;
Best Local Similarity 52.6%; Pred. No. 2.3e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCAGC 19
|||||
Db 4 CCAATCTGTCGCGCCAGC 22

RESULT 24 124 bp DNA linear GSS 23-AUG-2000
AA073902
LOCUS EP(3)3309-5prime Drosophila melanogaster EP line Drosophila
DEFINITION melanogaster genomic Sequence recovered from 5' end of P element,
DNA sequence.

ACCESSION AA073902
VERSION AA073902.1 GI:3403944
KEYWORDS GSS.
SOURCE fruit fly.

ORGANISM

Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 124)
Liao G.-C., Rehm E.J. and Rubin G.M.
Insertion site preferences of the P transposable element in
Drosophila melanogaster
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)

JOURNAL MEDLINE
COMMENT
Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-3200, USA
Fax: 5106439947
Email: gerry@fruitfly.berkeley.edu

Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element

The P element insertion position is base 117 in the 124 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon-tagged.
Location/Qualifiers
1. 124
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains a single EP
transposable element insertion. (The generation of these
insertion strains is described in North P, Szabo K, Bailey
A, Laverly T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes

FEATURES

SOURCE

V, Ansoorge W, Cohen SM, 1998. Systematic gain-of-function genetics in *Drosophila*. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitfly.berkeley.edu/P-distrupt/inverse_pcr.html.

BASE COUNT 26 a 44 c 21 g 33 t
 Query Match 52.6%; Score 10; DB 17; Length 124;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 85 CCAATTAATCATTCACG 103

RESULT 25
 BH812753/c
 LOCUS 124 bp DNA linear GSS 02-MAY-2002
 DEFINITION SALK_063023 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 ACCSSION BH812753
 VERSION BH812753.1 GI:20391208
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab
 , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 A5909620.
 Class: TDNA tagged.

FEATURES

source Location/Qualifiers
 1..124
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_063023"
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 29 a 13 c 39 g 43 t
 ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 124;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 117 CCAATAGTTATTCACG 99

RESULT 26
 BH847929/c
 LOCUS 124 bp DNA linear GSS 13-JUN-2002
 DEFINITION SALK_066091.36.55.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_066091.36.55.x, DNA
 sequence.

ACCESSION BH847929.1 GI:21418800
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab
 , C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.

TITLE
 JOURNAL
 COMMENT

FEATURES
 source Location/Qualifiers
 1..124
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_066091.36.55.x"
 /note="PCR was performed on Arabidopsis thaliana TDNA insertion lines"
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 38 a 20 c 35 g 31 t
 ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 124;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 116 CCAATTAATCATTCACG 98

RESULT 27
 AZ919927/c
 LOCUS 129 bp DNA linear GSS 17-DEC-2001
 DEFINITION 1006017C09.xl 1006 - RescueMu Grid G Zea mays genomic, DNA
 sequence.
 ACCSSION AZ919927
 VERSION AZ919927.1 GI:13390126
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 Waldbol,V.
 Maize genomic sequences found using engineered RescueMu transposon

JOURNAL
 COMMENT
 Unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1006017 row: 37
 Class: transposon-tagged.
 Location/Qualifiers
 source
 1.129
 /organism="Zea mays"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /clone_lib="1006 - RescueMu Grid G"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf. Vector: RescueMu (engineered from pBluescript backbone). Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.jastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT
 29 a 34 c 48 g 18 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 129;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 101 CCAATCCCGCCGCCACG 83

RESULT 28
 BH895687 130 bp DNA linear GSS 14-AUG-2002
 LOCUS 3526.1.35.1-C06.2EL.X_1 3526 - RescueMu Grid K Zea mays genomic,
 DEFINITION DNA sequence.
 ACCESSION BH895687
 VERSION BH895687.1 GI:22229898
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 130)
 Walbot, V.
 Maize genomic sequences found using engineered RescueMu transposon
 unpublished (2001)
 Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 3526.1.35.1 row: 27
 Class: transposon-tagged.

FEATURES
 source
 Location/Qualifiers
 1.130
 /organism="Zea mays"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /clone_lib="3526 - RescueMu Grid K"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf. Vector: RescueMu (engineered from pBluescript backbone). Site.1: BamHI; Site.2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.jastate.edu' and follow the links for 'RescueMu.' Grid K was grown at Molokai, Hawaii in Winter 2000-2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT
 20 a 63 c 29 g 18 t

ORIGIN

Query Match 52.6%; Score 10; DB 17; Length 130;
 Best Local Similarity 52.6%; Pred. No. 2.3e+04;
 Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 ||||| |||||
 Db 34 CCAATCGTGTGCGTCACG 52

RESULT 29
 BE936064 132 bp mRNA linear EST 02-OCT-2000
 LOCUS QV2-NN0054-230800-333-g09 NN0054 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BE936064
 ACCESSION BE936064.1 GI:10462140
 VERSION
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 132)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
 M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPER/P/LCR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=6t2=QV2-NN0054-230
 800-333-g09&t3=2000-08-23&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 132.
 Location/Qualifiers
 1.132
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

```

/clone_lib="NN0054"
/dev_stage="Adult"
/organism="Homo sapiens"
/site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      46 a      27 c      31 g      28 t
ORIGIN

```

```

Query Match      52.6%; Score 10; DB 12; Length 132;
Best Local Similarity 52.6%; Pred. No. 2.4e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

QY      1 CCAATNNNNNNNNCCACG 19
        |||||
Db      27 CCAATTGACACCTCCACG 45

```

```

RESULT 30
BF361951      132 bp      mRNA      linear      EST 24-NOV-2000
LOCUS      QV2-NN0042-210800-310-d07 NN0042 Homo sapiens cDNA, mRNA sequence.
DEFINITION      BF361951
ACCESSION      BF361951.1 GI:11323976
VERSION      EST.
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 132)
              Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
              M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.

```

```

TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

```

```

JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
COMMENT

```

```

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&lt2=QV2-NN0042-
210800-310-d07&lt3=2000-08-21&lt4=1)
Seq primer: puc 18 forward
High quality sequence stop: 132.

```

FEATURES

```

Location/Qualifiers
1..132

```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"

```

```

/clone_lib="NN0042"
/dev_stage="Adult"

```

```

/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      40 a      37 c      29 g      26 t
ORIGIN

```

```

Query Match      52.6%; Score 10; DB 12; Length 132;
Best Local Similarity 52.6%; Pred. No. 2.4e+04;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

QY      1 CCAATNNNNNNNNCCACG 19
        |||||
Db      46 CCAATTCCTGACACACACG 64

```

```

Search completed: November 16, 2002, 03:32:34
Job time : 1980 secs

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2002, 02:59:22 : Search time 47 Seconds
(without alignments)
149.377 Million cell updates/sec

Title: US-09-606-804-1

Perfect score: 19 ccaatnnnnnnccacg 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 328367 seqs, 184756068 residues

Total number of hits satisfying chosen parameters: 656734

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 90 summaries

Database :

Published Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCRTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	52.6	25	US-09-402-100-35	Sequence 35, App1
2	10	52.6	100	US-09-969-773-1152	Sequence 1152, Ap
3	10	52.6	123	US-09-867-701-3962	Sequence 3962, Ap
4	10	52.6	210	US-09-974-300-8096	Sequence 8096, Ap
5	10	52.6	214	US-09-778-320-59	Sequence 59, App1
6	10	52.6	214	US-09-910-689-59	Sequence 59, App1
7	10	52.6	214	US-10-010-742-59	Sequence 59, App1
8	10	52.6	219	US-09-783-590-10136	Sequence 10136, A
9	10	52.6	237	US-09-777-564-1013	Sequence 1013, Ap
10	10	52.6	238	US-09-960-352-13155	Sequence 1315, A
11	10	52.6	247	US-09-878-574-6181	Sequence 6181, Ap
12	10	52.6	261	US-09-604-387A-206	Sequence 206, App
13	10	52.6	261	US-09-339-338-206	Sequence 206, App
14	10	52.6	261	US-10-007-805-206	Sequence 206, App
15	10	52.6	262	US-10-033-528-1836	Sequence 1836, Ap
16	10	52.6	267	US-09-294-0938-1896	Sequence 1896, Ap
17	10	52.6	268	US-09-923-876-5857	Sequence 5857, Ap
18	10	52.6	271	US-09-783-590-11139	Sequence 11139, A
19	10	52.6	274	US-09-867-701-5278	Sequence 5278, Ap

20	10	52.6	280	US-09-878-574-246	Sequence 246, App
21	10	52.6	283	US-09-294-0938-3259	Sequence 3259, Ap
22	10	52.6	293	US-09-294-0938-6179	Sequence 6179, Ap
23	10	52.6	306	US-09-974-300-8100	Sequence 8100, Ap
24	10	52.6	339	US-09-878-574-1186	Sequence 1186, Ap
25	10	52.6	351	US-09-938-842A-1451	Sequence 1451, Ap
26	10	52.6	358	US-09-728-444-594	Sequence 594, App
27	10	52.6	363	US-09-770-791-478	Sequence 478, App
28	10	52.6	365	US-09-653-817-177	Sequence 177, App
29	10	52.6	367	US-09-878-574-2907	Sequence 2907, Ap
30	10	52.6	373	US-09-867-701-6841	Sequence 6841, Ap
31	10	52.6	381	US-09-878-574-2423	Sequence 2423, Ap
32	10	52.6	383	US-09-878-574-1113	Sequence 1113, Ap
33	10	52.6	389	US-09-960-352-5604	Sequence 5604, Ap
34	10	52.6	392	US-09-884-441-372	Sequence 372, App
35	10	52.6	396	US-09-930-300A-1484	Sequence 1484, Ap
36	10	52.6	399	US-10-033-528-1484	Sequence 1484, Ap
37	10	52.6	402	US-09-878-574-4036	Sequence 4036, Ap
38	10	52.6	405	US-09-878-574-3909	Sequence 3909, Ap
39	10	52.6	405	US-09-969-708-35	Sequence 35, App1
40	10	52.6	405	US-09-974-300-8367	Sequence 8367, Ap
41	10	52.6	411	US-09-938-842A-4215	Sequence 4215, Ap
42	10	52.6	418	US-09-919-580-485	Sequence 485, App
43	10	52.6	419	US-09-983-965-2492	Sequence 2492, App
44	10	52.6	437	US-09-920-300A-500	Sequence 500, App
45	10	52.6	437	US-10-033-528-500	Sequence 500, App
46	10	52.6	439	US-09-770-444-941	Sequence 941, App
47	10	52.6	440	US-09-895-828-293	Sequence 293, App
48	10	52.6	442	US-09-960-352-4377	Sequence 4377, App
49	10	52.6	445	US-09-878-574-4615	Sequence 4615, Ap
50	10	52.6	458	US-09-925-300-794	Sequence 794, App
51	10	52.6	460	US-09-864-761-22182	Sequence 22182, A
52	10	52.6	463	US-09-878-574-4545	Sequence 4545, Ap
53	10	52.6	476	US-09-864-761-14174	Sequence 14174, A
54	10	52.6	476	US-09-783-590-11499	Sequence 11499, A
55	10	52.6	480	US-09-864-761-11304	Sequence 11304, A
56	10	52.6	488	US-09-783-590-84	Sequence 84, App1
57	10	52.6	510	US-09-920-300A-1592	Sequence 1592, Ap
58	10	52.6	510	US-10-033-528-1592	Sequence 1592, Ap
59	10	52.6	512	US-09-919-580-844	Sequence 844, App
60	10	52.6	512	US-09-783-590-9422	Sequence 9422, App
61	10	52.6	518	US-09-998-598-130	Sequence 33, App1
62	10	52.6	519	US-09-919-580-140	Sequence 140, App
63	10	52.6	529	US-09-998-598-2598	Sequence 2598, App
64	10	52.6	531	US-09-604-287A-123	Sequence 123, App
65	10	52.6	531	US-09-339-338-123	Sequence 123, App
66	10	52.6	533	US-10-007-805-123	Sequence 123, App
67	10	52.6	533	US-09-919-580-351	Sequence 351, App
68	10	52.6	534	US-09-919-580-483	Sequence 483, App
69	10	52.6	534	US-09-920-300A-633	Sequence 633, App
70	10	52.6	534	US-10-033-528-633	Sequence 633, App
71	10	52.6	536	US-09-919-580-593	Sequence 593, App
72	10	52.6	537	US-09-919-580-236	Sequence 236, App
73	10	52.6	537	US-09-919-580-518	Sequence 518, App
74	10	52.6	541	US-09-919-580-502	Sequence 502, App
75	10	52.6	550	US-09-813-358-191	Sequence 191, App
76	10	52.6	553	US-09-833-381-1568	Sequence 1568, Ap
77	10	52.6	555	US-09-924-033A-140	Sequence 140, App
78	10	52.6	556	US-09-919-580-316	Sequence 316, App
79	10	52.6	556	US-09-919-580-556	Sequence 556, App
80	10	52.6	553	US-09-917-800A-825	Sequence 825, App
81	10	52.6	564	US-09-919-580-310	Sequence 310, App
82	10	52.6	564	US-09-919-580-535	Sequence 533, App
83	10	52.6	567	US-09-919-580-335	Sequence 339, App
84	10	52.6	570	US-09-919-580-468	Sequence 468, App
85	10	52.6	573	US-09-919-580-360	Sequence 360, App
86	10	52.6	579	US-09-919-580-227	Sequence 227, App
87	10	52.6	579	US-09-919-580-560	Sequence 560, App
88	10	52.6	588	US-09-864-761-8882	Sequence 8882, App
89	10	52.6	595	US-09-814-292-45	Sequence 45, App1
90	10	52.6	599	US-09-864-761-8472	Sequence 8472, App

ALIGNMENTS

RESULT 1

US-09-402-100-35/c
; Sequence 35, Application US/09402100
; Patent No. US20010019834A1
; GENERAL INFORMATION:
; APPLICANT: Daewoong Pharmaceutical Co, LTD
; APPLICANT: Kim, Byung-O
; APPLICANT: Shin, Sung-Seup
; APPLICANT: Yu, Young-Hyo
; APPLICANT: Park, Myung-Hwan
; APPLICANT: Choi, Deok-Joon
; APPLICANT: Jung, Hyung-Jin
; TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Helicobacter
; FILE REFERENCE: 0136/0G140
; CURRENT FILING DATE: 1999-09-27
; EARLIER FILING DATE: 1997-03-31
; EARLIER APPLICATION NUMBER: KR 97-11950
; EARLIER FILING DATE: 1997-03-31
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: Oligonucleotide
US-09-402-100-35

Query Match

Best Local Similarity 52.6%; Score 10; DB 10; Length 25;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

Db 20 CCAATTTTTCATCCACG 2

RESULT 2

US-09-969-373-1152/c
; Sequence 1152, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Efferetz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1152
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1152

Query Match

Best Local Similarity 52.6%; Score 10; DB 10; Length 100;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

Db 97 CCAATCATTTCCATCCACG 79

RESULT 3

US-09-867-701-3962
; Sequence 3962, Application US/09867701
; Patent No. US2002013237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3962
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-3962

Query Match

Best Local Similarity 52.6%; Score 10; DB 10; Length 123;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

Db 4 CCAATCTGTCGACGACG 22

RESULT 4

US-09-974-300-8096/c
; Sequence 8096, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US/09/974,300
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8096
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(210)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-8096

Query Match

Best Local Similarity 52.6%; Score 10; DB 10; Length 210;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19

Db 152 CCAATTTGCTGTCACG 134

RESULT 5

US-09-778-320-59/c

```

Sequence 59, Application US/09778320
Patent No. US20010034052A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yuqiu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778,320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 214
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(214)
OTHER INFORMATION: n = A,T,C or G
US-09-778-320-59

```

```

Query Match      52.6%; Score 10; DB 10; Length 214;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAGC 19
    ||||| |||||
DB 88 CCAATCTTCATCTCCAGC 70

```

```

RESULT 6
US-09-910-689-59/C
Sequence 59, Application US/09910689
Patent No. US20020081609A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yuqiu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C6
CURRENT APPLICATION NUMBER: US/09/910,689
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 214
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 34, 120, 153, 159, 171, 179, 184, 194, 197
OTHER INFORMATION: n = A,T,C or G
US-09-910-689-59

```

```

Query Match      52.6%; Score 10; DB 10; Length 214;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

```

```

OY 1 CCAATNNNNNNNNCCAGC 19
    ||||| |||||
DB 88 CCAATCTTCATCTCCAGC 70

```

```

RESULT 7
US-10-010-742-59/C
Sequence 59, Application US/10010742
Patent No. US20020146727A1
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yuqiu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
APPLICANT: Bennington, Angela Ann
APPLICANT: Zehentner, Barbara
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C7
CURRENT APPLICATION NUMBER: US/10/010,742
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 214
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 34, 120, 153, 159, 171, 179, 184, 194, 197
OTHER INFORMATION: n = A,T,C or G
US-10-010-742-59

```

```

Query Match      52.6%; Score 10; DB 12; Length 214;
Best Local Similarity 52.6%; Pred. No. 3.9e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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OY 1 CCAATNNNNNNNNCCAGC 19
    ||||| |||||
DB 88 CCAATCTTCATCTCCAGC 70

```

```

RESULT 8
US-09-783-590-10136
Sequence 10136, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Steven M.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16 2C1
CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10136
LENGTH: 219
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (3)
OTHER INFORMATION: n equals a,t,g, or c

```

```
NAME/KEY: misc feature
LOCATION: (17)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (19)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (36)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (48)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (134)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (145)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (150)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (182)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (186)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (187)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (205)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-10136
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 219;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 CCAATNNNNNNNNCCAG 19
Db 99 CCAATACACACACCCAG 117
```

```
RESULT 9
US-09-777-564-1013
Sequence 1013, Application US/09777564
Patent No. US20020022591A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: Mammion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
NUMBER OF SEQ ID NOS: 2001-02-05
SOFTWARE: FastSeq for Window Version 4.0
SEQ ID NO 1013
LENGTH: 237
TYPE: DNA
ORGANISM: Homo sapiens
US-09-777-564-1013
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 237;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCAG 19
Db 18 CCAATTCAGCCTGCCAG 36
```

```
RESULT 10
US-09-960-352-13155/C
Sequence 13155, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nadappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 1511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 2001-09-24
SEQ ID NO 13155
LENGTH: 238
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 56-LIB34-004-Q1-E1-F8
US-09-960-352-13155
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 238;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 CCAATNNNNNNNNCCAG 19
Db 159 CCAATATGTTAGATCCAG 141
```

```
RESULT 11
US-09-878-574-6181/C
Sequence 6181, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Hyrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
NUMBER OF SEQ ID NOS: 1995-06-14
SEQ ID NO 6181
LENGTH: 247
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701097950H1
US-09-878-574-6181
```

```
Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 247;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 CCAATNNNNNNNNCCAG 19
Db 242 CCAATACCTGTTCCAG 224
```

```
RESULT 12
US-09-604-287A-206
Sequence 206, Application US/09604287A
Patent No. US20020064872A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yudi
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
```



```

; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-604-287A-206

```

```

Query Match          52.6%; Score 10; DB 10; Length 261;
Best Local Similarity 52.6%; Pred. No. 4e+02; 9; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 9;

```

```

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
DB 140 CCAATCTTCATCTCCACG 158

```

```

RESULT 13
US-09-339-338-206
; Sequence 206, Application US/09339338A
; Patent No. US20020102602A1
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-339-338-206

```

```

Query Match          52.6%; Score 10; DB 10; Length 261;
Best Local Similarity 52.6%; Pred. No. 4e+02; 9; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 9;

```

```

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
DB 140 CCAATCTTCATCTCCACG 158

```

```

RESULT 14
US-10-007-805-206
; Sequence 206, Application US/10007805
; Patent No. US20020150581A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vegdick, Thomas S.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Durham, Margarita
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.470C10

```

```

; CURRENT APPLICATION NUMBER: US/10/007,805
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 593
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-805-206

```

```

Query Match          52.6%; Score 10; DB 12; Length 261;
Best Local Similarity 52.6%; Pred. No. 4e+02; 9; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 9;

```

```

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
DB 140 CCAATCTTCATCTCCACG 158

```

```

RESULT 15
US-10-033-528-1836
; Sequence 1836, Application US/10033528
; Patent No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeline Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1836
; LENGTH: 262
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1836

```

```

Query Match          52.6%; Score 10; DB 12; Length 262;
Best Local Similarity 52.6%; Pred. No. 4.1e+02; 9; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 9;

```

```

QY 1 CCAATNNNNNNNNCCACG 19
    |||||
DB 144 CCAATCTTCATCTCCACG 162

```

```

RESULT 16
US-09-294-093B-1896
; Sequence 1896, Application US/09294093B
; Patent No. US20010051335A1
; GENERAL INFORMATION:
; APPLICANT: Ito, Laura, Y.
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US
; CURRENT APPLICATION NUMBER: US/09/294,093B
; CURRENT FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/082,567
; PRIOR FILING DATE: April 21, 1998
; NUMBER OF SEQ ID NOS: 6207
; SOFTWARE: PERL Program
; SEQ ID NO 1896
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20010051335A1 700345158H1

```

NAME/KEY: unsure
LOCATION: 8, 24, 45, 69, 106, 174, 192, 197, 199-200, 206-207, 209, 227, 257, 260
OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-1896

Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 267;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 214 CCAATCGCGGCGGCCACG 232

RESULT 17
US-09-923-876-5857
Sequence 5857, Application US/09923876
Patent No. US20020013958A1
GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Itc)
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
PRIORITY FILING DATE: 2001-08-06
PRIORITY FILING DATE: 1999-04-21
PRIORITY FILING DATE: 1999-04-21
PRIORITY FILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program
SEQ ID NO 5857
LENGTH: 268
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700457860H1
LOCATION: 65, 202, 216
OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-5857

Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 268;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 9 CCAATCGCGGCGGCCACG 27

RESULT 18
US-09-783-590-11139/c
Sequence 11139, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16,2C1
CURRENT APPLICATION NUMBER: US/09/783,590
PRIORITY FILING DATE: 2000-02-15
PRIORITY FILING DATE: 1995-04-12
PRIORITY FILING DATE: 1995-04-12
PRIORITY FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11139
LENGTH: 271
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (7)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (20)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (56)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (92)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (216)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (223)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (251)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (253)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (258)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (259)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (266)
OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-11139

Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 271;
Matches 11; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
DB 102 CCAATCGGTTAAACACG 84

RESULT 19
US-09-867-701-5278/c
Sequence 5278, Application US/09867701
Patent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
PRIORITY FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5278
LENGTH: 274
TYPE: DNA
ORGANISM: Homo sapien
US-09-867-701-5278

Query Match
Best Local Similarity 52.6%; Score 10; DB 10; Length 274;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 |||||
 Db 150 CCAATTAACAGGCCACG 132

RESULT 20

US-09-878-574-246
 ; Sequence 246, Application US/09878574
 ; Patent No. US20020110548A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Byrum, Joseph R.
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Thompson, Michael D.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; FILE REFERENCE: 38-21(15401)B
 ; CURRENT APPLICATION NUMBER: US/09/878,574
 ; PRIOR FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: 09/333,535
 ; PRIOR FILING DATE: 1999-06-14
 ; NUMBER OF SEQ ID NOS: 15775
 ; SEQ ID NO 246
 ; LENGTH: 280
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: LIB3028-053-Q1-B1-D5
 US-09-878-574-246

Query Match 52.6%; Score 10; DB 10; Length 280;
 Best Local Similarity 52.6%; Pred. No. 4.1e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 |||||
 Db 135 CCAATCATCATGCACG 153

RESULT 21

US-09-294-093B-3259
 ; Sequence 3259, Application US/09294093B
 ; Patent No. US20010051335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalquid, Raghunath, V.
 ; APPLICANT: Ito, Laura, Y.
 ; APPLICANT: Sherman, Bradley, K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
 ; FILE REFERENCE: PL-0009 US
 ; CURRENT APPLICATION NUMBER: US/09/294,093B
 ; PRIOR FILING DATE: 1999-04-16
 ; PRIOR APPLICATION NUMBER: 60/082,567
 ; PRIOR FILING DATE: April 21, 1998
 ; NUMBER OF SEQ ID NOS: 6207
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 3259
 ; LENGTH: 283
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20010051335A1 70037672H1
 ; LOCATION: 33, 53
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-294-093B-3259

Query Match 52.6%; Score 10; DB 10; Length 283;
 Best Local Similarity 52.6%; Pred. No. 4.1e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 |||||
 Db 4 CCAATCCCTTCCACG 22

RESULT 22

US-09-294-093B-6179
 ; Sequence 6179, Application US/09294093B
 ; Patent No. US20010051335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lalquid, Raghunath, V.
 ; APPLICANT: Ito, Laura, Y.
 ; APPLICANT: Sherman, Bradley, K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
 ; FILE REFERENCE: PL-0009 US
 ; CURRENT APPLICATION NUMBER: US/09/294,093B
 ; PRIOR FILING DATE: 1999-04-16
 ; PRIOR APPLICATION NUMBER: 60/082,567
 ; PRIOR FILING DATE: April 21, 1998
 ; NUMBER OF SEQ ID NOS: 6207
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 6179
 ; LENGTH: 293
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20010051335A1 700383150H1
 ; LOCATION: 280, 255-256
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-294-093B-6179

Query Match 52.6%; Score 10; DB 10; Length 293;
 Best Local Similarity 52.6%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 |||||
 Db 54 CCAATATCTATTGCCACG 72

RESULT 23

US-09-974-300-8100
 ; Sequence 8100, Application US/09974300
 ; Patent No. US20020146721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Clausen, Id Groth
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
 ; FILE REFERENCE: 10085,500-US
 ; CURRENT APPLICATION NUMBER: US/09/974,300
 ; PRIOR FILING DATE: 2001-10-05
 ; PRIOR APPLICATION NUMBER: 09/680,598
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/279,526
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 8481
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8100
 ; LENGTH: 306
 ; TYPE: DNA
 ; ORGANISM: Bacillus clausii
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)-(306)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-974-300-8100

Query Match 52.6%; Score 10; DB 10; Length 306;
 Best Local Similarity 52.6%; Pred. No. 4.2e+02;

Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
 |||||

Db 94 CCAATTCGCTGTCCACG 112

RESULT 24

US-09-878-574-1186/C
; Sequence 1186, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878, 574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333, 535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 1186
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-041-Q1-B1-A12
US-09-878-574-1186

Query Match 52.6%; Score 10; DB 9; Length 339;
Best Local Similarity 52.6%; Pred. No. 4.3e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 164 CCAATGAATGTAACACG 146

RESULT 25

US-09-938-842A-1451/C
; Sequence 1451, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1451
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1451

Query Match 52.6%; Score 10; DB 9; Length 351;
Best Local Similarity 52.6%; Pred. No. 4.3e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 143 CCAATCAGAGCTGCCACG 125

RESULT 26
US-09-728-444-594/C

; Sequence 594, Application US/09728444
; Patent No. US20020161207A1
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Friedreich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: and Murine Polynucleotide Sequences
; FILE REFERENCE: LEX-0100-USA
; CURRENT APPLICATION NUMBER: US/09/728, 444
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168, 360
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 1206
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(358)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-444-594

Query Match 52.6%; Score 10; DB 9; Length 358;
Best Local Similarity 52.6%; Pred. No. 4.3e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 95 CCAATCTCCAAGCCACG 77

RESULT 27

US-09-770-791-478
; Sequence 478, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Mathew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kitzner, Maya
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hoffman, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770, 791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178, 480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-478

Query Match 52.6%; Score 10; DB 10; Length 363;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 105 CCAATCAGCTCAGCCACG 123

RESULT 28
US-09-563-817-177
; Sequence 177, Application US/09563817
; Patent No. US20020095031A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020095031A1e1 Human Polynucleotides and the
; FILE REFERENCE: LEX-0021-USA
; CURRENT APPLICATION NUMBER: US/09/563,817
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/132,343
; PRIOR FILING DATE: 1999-05-04
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 177
; LENGTH: 365
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(365)
; OTHER INFORMATION: n = A,T,C or G
US-09-563-817-177

Query Match 52.6%; Score 10; DB 10; Length 365;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 244 CCAATTCCTCATCCACG 262

RESULT 29
US-09-878-574-2907
; Sequence 2907, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 2907
; LENGTH: 367
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-018-Q1-H1-D9
US-09-878-574-2907

Query Match 52.6%; Score 10; DB 10; Length 367;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CCAATNNNNNNNNCCACG 19

Db 197 CCAATCAGCTGAGCCACG 215
|||||

RESULT 30
US-09-867-701-6841/c
; Sequence 6841, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aqlate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Hailocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6841
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-6841

Query Match 52.6%; Score 10; DB 10; Length 373;
Best Local Similarity 52.6%; Pred. No. 4.4e+02;
Matches 10; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 CCAATNNNNNNNNCCACG 19
|||||
Db 202 CCAATATAGTAAACCACG 184

Search completed: November 16, 2002, 04:29:24
Job time : 49 secs

